STIC-Biotech/ChemLib

From: Sent:

Ibrahim, Medina A.

Monday, September 12, 2005 11:02 AM

To: Subject: STIC-Biotech/ChemLib 10/713,381

Please search the following:

- 1. SEQ ID NO: 1 and 2.
- 2. the sequence from nucleotide position 1 to nucleotide position 1311 of SEQ ID NO: 1 or 2.
- 3. the sequence from nucleotide position 1155 to nucleotide position 1311 of SEQ ID NO: 1 or 2.
- 4. the sequence from nucleotide position 1179 to nucleotide position 1208 of SEQ ID NO: 1 or 2.
- 5. the sequence from nucleotide position 1239 to nucleotide position 1278 of SEQ ID NO: 1 or 2.
- 6. an oligo of SEQ ID NO: 1 or 2.

Please search both commercial and patent (including pending) databases. Thanks

Medina A. Ibrahim Patent Examiner, GAU-1638 transgenic plants and plant breeding Remsen-2B07 mailbox-2C18 (571) 272-0797

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Type o	of Search
(Y)	/
NA#:	AA#:
Interference:	SPDI:
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Inventor:	Litigation:

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REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM LOCUS DEFINITION ACCESSION RESULT 1 AX224394 FEATURES source VERSION JOURNAL Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 1 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers AX224394 1394 bp Sequence 1 from Patent W00160997. AX224394 AX224394.1 GI:15554636 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. **Zea mays** Zea mays /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" DNA linear and Kendall, T.L. of using same PAT 10-SEP-2001

ALIGNMENTS

1261 CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311 	1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260 	1141 GGTTCGGCAGCTCTCGTGTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200 	1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140 	1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC 1080 	961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 	901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTAAT	841 TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900 	781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780	661 ATTGTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720 	601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT 660	181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCCATCAAGGGCCTTTCGGATGGCCCA 240 241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA 300
Qy 601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT 660	Qy 541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 600	Qy 481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540	Qy 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAAATAACCAAAGTAACTAATCCACT 480	Qy 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420	Qy 301 TTATTATICTTTAGATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTTGTGTA 360	OY 241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA 300	Qy 181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	Qy 121 CTCCATGTTCCACCTTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	QY 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	Qy 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	Query Match 100.0%; Score 1311; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 3.6e-252; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 2 AX224395 LOCUS LOCUS Sequence 2 from Patent WOO160997. ACCESSION AX224395.1 GI:15554637 VERSION KEYWORDS SOURCE Cae mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD AUTHORS AUTHORS AUTHORS ALBertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L. Batent: WO 0160997-A 2 23-AUG-2001; FEATURES FEATURES FEATURES FEATURES FOURCE 11394 /mol_type="unassigned DNA" /db_xref="taxon:4577"

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PF 19-JUN-1998 JP 199504910
PF 29-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W PI TIMMY L KENDALL
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 3.0
tive 0; Mismatches
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Query Match Query Match 100.0%; Score 1311; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 3.6e-252; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	PF 19-JUN-1998 JP 199504910 PR 23-JUN-1997 US 08/880499 PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFWAN, PI TIMMY L KENDALL PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC CC Strandedness: Single; CC Topology: Linear; CC Topology: Linear; FH Key Location/Qualifiers FEATURES FOURCE 1.1394 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	RESULT 4 BD062177 LOCUS LOCUS DEFINITION Male tissue-preferred regulatory region and method of using same. ACCESSION MO62177.1 GI:22607782 KEYWORDS SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall,T.L. TITLE JOURNAL Patent: JP 2001520523-A 2 30-OCT-2001; PD 30-OCT-2001	99 TIGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTTG 960
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1021 TTCTCTAGATTAGTAAAAGGGAGAGAGAGAGAGAATCAGTTTTAAGTCATTGTCCC 1080	781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTAAGAATTTTGATTT 840		61 CTTCTTCTGCCTTATTACTGAATCGGATTACAAAAACTTCCACGGGTGCATGAT 120 [

Query Match Best Local Similarity 100.0%; Score 1311; DB 8; Length 3343; Best Local Similarity 100.0%; Pred. No. 3.5e-252; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTC Db 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTC Qy 61 CTTCTTCTGCCTTATGAAAAAGATGAATGCGGGTTACAAAAAAACTTCCACGGGTGCATGA Db 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAAACTTCCACGGGTGCATGA	/produci = "male fertility protein" /db xxef="GI:14028757" /db xxef="GI:14028757" /translation="mekrancomragroryphiferanialityappeglsplaev /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompassivencynstyphiferanicompyaglappegls" /translation="mekrancompyaglappegls" /translation	/gene="M845" join(<1392. 1768,18982182,22802 /gene="M845" /product="male fertility protein" join(13921768,18982182,228024 /gene="M845" /codon at atti		S Fox,T.W., Trimnell,M.R. and Albertsen,M.C. Cloning of M845, a gene required for male fe. L. Unpublished E 2 (bases 1 to 3343) E 2 (bases 1 to 3343) S Fox,T.W., Trimnell,M.R. and Albertsen,M.C. Direct Submission L. Submitted (13-MAR-2001) Trait and Technology Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. IA 50131-1004, USA	AP360356.1 GI:14028756 AP360356.1 GI:14028756 . Zea mays Zea mays Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsid, clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 3343)	
; Length 3343; 2; Indels 0; Gaps 0; pharaccgrittctragggicc 60 [TAALALLUVADDEGLSPLAEV SVFGPESIEFDLQGRGPYAGLA FRKQHEKEEFCGRELGLREHGE FANDLDVHRNGSVFFTDTSMRY FPNGVQISEDHQFLLFSETTNC FVAIDCCRTPAQEVFAKREWLR TLEDRGHEVMKLVSEVREVGRK Db Db	.2447,2534>2942) Db 2447,25342942)	OV Db	rility from Zea mays Db Qy Development, Pioneer Db Box 1004, Johnston, Qy	gene, complete cds. Qy Db Embryophyta; Tracheophyta; Poales; Poaceae; PACCAD Db	1200 1260 1260
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Research, 320 Cnarry

B (bases 1 to 186199)

RS (bases 1 to 186199)

RS birren, B, Nusbaum, C., Lander, E., Butler, E., Wing, R., Bnarry, N., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Abouelleil, A., Allen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pherre, N., Hafez, N., Hagopian, D., Hagog, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Iliu, A., Mabbitt, R., MacLean, C., Macdonald, P., Matthews, C., McCarthy, M., Meldrim, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS Birren, B., Nuabaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArelland, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Raman, J., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stobbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Zea mays
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Submitted (19-DEC-2003) Whitehead Institute/MIT Center Submitted (19-DEC-2003) Whitehead Institute/MIT Center Sesearch, 320 Charles Street, Cambridge, MA 02141, USA
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Unpublished
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.
                                                                                                                                                                                                                                                    * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 100617: contig of 100617 bp in length

1 100718 100717: gap of unknown length

1 104731 104830: gap of unknown length

1 104731 115104: contig of 10274 bp in length

1 115105 115204: gap of unknown length

1 15205 156396: contig of 41192 bp in length

1 156497 179936: contig of 6163 bp in length

1 19937 180036: gap of unknown length

1 19937 180036: gap of unknown length

1 19938: contig of 63440 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 17, 2004 this sequence version replaced gi:49658659. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                CDS
                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162177 TITCCAAACTAACCCTCAAGTATATAATGAATGCAGGACAA 162217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162117
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                                                                                                                                                                                                                                                                                                                                           Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Feb 21, 2004 this sequence version replaced gi:19570016, gi:20087114.

CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (Dases 1 to 25769)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., D
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A.
                                                                                                                                                                                                                                                                                   is available from IMB Jena, Department of Genome Analy (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence and analysis of Nature 418 (6893), 79-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum chromosome AX4, complete sequence. AC117267 AC115597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baumgart,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baumgart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 25769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC117267.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTAAGTGAAATTAGTTCATTTTCTCTTAACAAAATAGAAATTTATTGGTAAAATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTTCTTTTACTTTTAGGGCTAGTTTGGGGAACCCTATTT-TTCTAAGAAATTTTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 25769)
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                                                                                                                                                                                                                         Deutsche Forschungsgemeinschaft Location/Qualifiers
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23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:42733680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%;
                                                                                                                                                                _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 77; DB 2;
Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 2 of Dictyostelium discoideum (2002)
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                                                           .1070,1237. .1349,1533. .1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NA linear INV 2;
2 map 5836255-5862024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pachebat, J., Dear, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INV 21-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kumpf, K., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SGC

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ARGROIDIGKNTAGYKNYIALVEKSKRKFTDFKTPNKNQVCSKRSWDGQIKKWRRQLH
ARGROIDIGKNTAGYKNYIALVEKSKRKFTDFKTPNKNQVCSKRSWDGQIKKWRRQLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEFPTKYVYITSNLDKPKEWFTQSEMSLTTTTDTIQKSFVNNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRLQIILFLSILLIFQLKSTFSSNDISSTILSITPNFNKDYNNQ
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complement(5711. .6796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGSGSSGTSGAQLSGTGYVINHQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAS38625.
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                                                                                                                                                                                                                                                                                                               (in
                                                                                                                                                                                                                                                                                                            order of location ranges):
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                                                                                                                                                                                                                                                                                                                                                    CDS
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SGC

CBS

SSSIVIKCEEQQQQQQQQQQQQQQQQQQQQQQQDGFLKSQEFPNLFKNKLYLKDDIS

CDS

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SQQPSPTIISQINHNKYQLFKEFKEHNNNIDSKMLCVQLSEFQISPKTATNTFDSWLN
SLMLPPTGFKKLVDNHLKKYYIPFYSYRVNYNVEFSGFVTYDSKLNTNALYDKYGNTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKCCVKIHCDEVCDLDCGRGFECKIRHDGSKCCVRSERPHPPQHEKCNKRCPPGHECK VDQHGKECCVVAHRPPPKCSLRCPPRHECRVNHFGEECCVKVHHDKCSLRCPPGHECK VDQHGKECCVVAHRPPPKCSLRCPPKHECRINHFGEECCVKSRNDCLTCEDLNCERKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCPIGHICVEDSNGVNCVPNGGGTSGGSSSTGTSGGHPDPCRDVDCPDGFHCECKDGK
TAKCVPSPTTGSSSTSGGHPDPCKDVTCPDGFHCECKDGKTAKCVPSPTTGSSSTSGG
NTNPCGNNNCPDGFYCECKDGKTAKCVPSGFTQPFKPPVCSLRCPPNHECKFDDDHG
CCVKVHHDRCSLRCPHGHECKVDHNGKECCVRSHRPPPEVCSLRCPPKHECKFDDHG
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QKNSCSNPTSCCPGESICEGLSSGSSTSGGGSSGGTSGGSSSGGTSGGSSSGGTSGSS
SSGSSSGGVSSCSTTHCPEGYHCSMVNDVATCLASTTGGTGLPGTSSSTAGVSSCLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (21961. .24357)
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join(16184. .16199,17272. .17613,17707. .19331)

join(e="GeneID exon scores (in order of location ranges):

0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
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frL1ENKTVNKEAISYYGLNYNQYQLLDEFTRLLKLKNKTTDCKNKIINTHNSLNKCC
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KTIELIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNSNKILSGIYFAHKKSKRY
                                                                                                                                                                                                                                                                                                                                                          /note="GeneID exon scores
173.48 - GSCJ_ID dd_00724"
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mold). Hypothetical 97.7 kDa protein"
/protein idd"AAS386630.1"
/db_xref="GI:42733686"
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/note="GeneID exon scores (in ord
2.42, 136.56 - GSCJ_ID dd_00727"
                                                                                                                                                                                                        /product="similar to Arabidopsis thaliana (Mouse-ear ress). Putative PREG1-like negative regulator"
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Matches 217; Conserv
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99108072
                                                                                                                                                                                                        Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 713)
Dechering, K. J., Kaan, A. M., Mbacham, W., Wirth, D. F., Eling, W., Koninge, R. N. and Stunnenberg, H. G.
Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite plasmodium falciparum
Mol. Cell. Biol. 19 (2), 967-978 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                     713
Plasmodium falciparum sexual
partial cds.
                                                                                       Submitted (12-NOV-1997) Molecular Toernooiveld 1, Nijmegen 6525 ED, Location/Qualifiers
                                                                                                                                            2 (bases 1 to 713)
Dechering, K.J., Kaan, A.M. and Konings, R.N.H.
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ĀF034389.1 GI:3098290
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         /organism="Plasmodium falciparum"
/mol_type="genomic DNA"
/strain="NF54"
/db_xref="taxon:5833"
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EQQSIEEETFIESSFEETKEVVEEVPFEEQFEILPISIGEETLKEYTSFLSVLSELIV
DMYNDDDKSSTSSQSSSSSSSSSAPSSPKPIKNNDNYTTTTTTTTTTTTTTTTSKTATSS
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Pred. No. 0.00015;
0; Mismatches 221;
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                                                                                                                                    TATCTATATATAAAA 67
                                                                                                                                                             GAGAGAGAGAAGAAA 1059
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/product="sexual stage ant
/protein id="AAD12581.1"
/db xref="GI:3098291"
/translation="M"
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537. .710
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537. .>713
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45.8%;
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Pred. No. 0.00045;
0; Mismatches 333;
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(migA) ge
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                                          linear
complete
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 3576)
1 (bases 1 to 3576)
Escalante, R., Weesels, D., Soll, D.R. and Loomis, W.F.
Chemotaxis to cAMP and slug migration in Dictyostelium both depend
on migA, a BTB protein
Mol. Biol. Cell 8 (9), 1763-1775 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-JAN-1997) Department of Biology, University of
California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                           /gene="migA"
/number=1
951. .1289
                                                                                                                                                                                                                                                                                                         /gene="migA"
/function="essential for slug migration"
/function="essential for slug migration"
/note="N-terminus of this protein is similar to other BTB
domain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
U14556 and L16896, respectively"
                                                                                                                                            melanogaster
                                                                                                                                                                                                                                                                    TNGEQWTVLKRHTNDPSLNYKYATHSWPVTGCETAFRYFRILQTGKNSNNRNFLVIGG
                                                                                                                                                                                                                                                                                  LKRYQPRPPQSILFEYSFDFDFKGIIFWISTDGGNEKWSNPHSTSKIKITSSSIDKGN
LYDIVELTPNAFWTKDVPASWVMIDLGPNRTVVPMYYTIRHGLSYKSDSLRTWDFQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="MigA"
/protein_id="AAB47544.1"
/db_xref="GI:1841872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /_____(<884. .2899,2998. .>3423)
/gene="migA"
/myzd:--
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             /number=1
2998. .>3423
                                                         /note="gene interruption
/replace="pbsr1 external
2900. .2997
                                                                                                                                                             /gene="migA"
/note="encodes
                                                                                                                                                                                                                                                    LEIYGELCETNPNPN"
/gene="migA"
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                                        gene="migA"
                                                                                                   gene="migA"
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chromosome="4"
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                                                                                                                    r U01333"
                                                                                                                                              BTB domain; similar to the Drosophila 
TB domain encoded by GenBank Accession
                                                                     in mutant"
plasmid, a
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                                                                     approximately 4
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                                                                                                                                                             Center code: SC
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149526 bp
Danio rerio clone CH211-117K16,
BX957346
Assembly program: KGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 149526 bases at least
Insert size: 149526; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                          BXS57346.13 GI:54019944
HTG; HTGS PHASE2; HTGS ACTIVEFIN; HTGS_DRAFT;
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 bases 1 to 149526)
                                                                                                                        Center project name: zC117K16
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ilarity 47.2%;
Conservative
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Pred. No. 0.00043;
0; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WORKING DRAFT SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; E
Ostariophysi;
                  Q20
Q20
Q20
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DEFINITION
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                                                              RESULT 13
PFMAL4P1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 TATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAAACAAGCAT 547
PFMAL4P1 347582 bp Plasmodium falciparum MAL4P1. AL034557 AL844503
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Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
coverage: 12.54x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                    CAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTGGCC
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                                                                                                                                                                                                                                             AGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the finished sequence as soon as it is
the accession number will be preserved.
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clone_end:T7
vector_side:left"
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/db_xref="taxon:7955"
/clone="CH211-117K16"
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                                            INV 29-JAN-2003
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 347582)
Hamlin,N., Pain,A., Berriman,B.,
Harris,B., Harris,D., Lawson,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall, N., Pain, A., Berriman, M., Churcher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1SA, UK
/db_xref="Q3.2320"
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GASGDAKNYIDDLKGDLQXABNINPKLIGTDDPCKLVEDYYNNHVNGDGKGKTRYPCTE
LSGKKFQNPFSDTLGGQCTNSKMRSGCEGACAPYRLHLCHHNLESIETTSKTASDTL
LLEVCMAAKYEGQSINTHYTKHEHSNKDSFSQLCTVLARSFADIGDIVRGKDLFYGNT
YESARREKLENKLKEVPGKIHGGLSEEAKKKYQDGDGNYYQLREDWMTANRETVWKAI
TCEVKSGNNYFRATGCDEKNPSITSKQCRCDKDKAGKFIKGSGNNIVIPTYFDYVPQY
LRWPEEWAEDPFCRLRHKLKDAIKKCRGKNGESKYCDLNRYDCKNTASGKHVFEBPB
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KKFYKELKGTKYKVNNPLEKLNDEDVCTKNNDIKDGGNIDFKMYHSGSAKKGDGNNK
TFYRTKYCEACPWGAEKVEGGWKAKEENCSQTKDYDPDKTTTIEILTGDTRKSDMVQ
KYKKFCNGNGGNGEKSATPNATSREKGKKGDQMEKMICYYDENKEKKYGSDAINFCVL
KONTANTONYTTTONYTTTONYTTTONYTTTONYTTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTONYTTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similar to Plasmodium falciparum variant-specific
surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa
fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: PFD0005w"
join(35153. .41725,42757. .44124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="rep20 Repeats"
join(35153..41725,42757./gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_id="CAD49094.1"
/db_xref="GI:23498127"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /isolate="3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="MAL4P1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hall, N.,
Quail, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .44124)
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and Barrell, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Churcher, C.,
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EKGLDAEBAKEIKHLROMLEQAGVRDLAAVGGPCTEGGVAEQNTIMDKFLDEELKEAE CKNCPK KAQQEGPGARSADSPAGTEDHPDAEDDDDEDDEDEEEEEEEE PQCKVPKTEATEDBRYKOVGDCHEKVYGKNGPDWKCGDLTLUDDTKVCWPPRROKLCL YYIAHESETKNIETODDLRDAFIRTAAAETFLSWQYYKIKNGADAKQLDNGTIPEEFL

EWGEEFCAERGKLEQNIGKSCNGINPIQYSCDNRHCDKKACDEYKNYVETKOKEPROD EWGEEFCAERGKLEQNIGKSCNGINPIQYS DDNRHCNKACDEYKNYVETKOKEPROD

TTKFVRDANLENADGYTUV TTTGGFS (GONDYLING CONTROLL ISSTGNYTKVTEFVNTIYSKYNGTCNLMRSSINPTACYTIETELSIKTGGAGTGDHPP LYAIRQMIKGLAEEATEAAKAAEAAKNAKLTAAIKEKQTALIEAGFNSSITSINASII AILIIVLIMVIIYLILRYRRKKKMKKKLQYIKLLKE" Similar to Plasmodium falciparum rifin pfb0030C SWALL:096112 (EMBL:AE001367) (370 aa) fasta sco /note="1 probable transmembrane helix predicted by TMHNM2.0 at aa 328-350 APATYDDDPQMKEVMVKFSKQTQQRFHEYDERMVEKRMQCKDKCDKEIQKIILKDKME KELMDKFATLQTDIQSDAIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGSVAV HVWKPKALEAAIAKAIAEGTADIAAAAEAAGKARGMEFVIKALKHFGVENFFPGICDT NTTASGNNTTASGKNTPSDTQNDIQSDGIPSSKITDNEWNTLKDEFISQYIQSEQPKD VPNDYSSGDIPFNTQHNTLYFDKPDEKPFITSIHDRNLYTGEEYNYDMSTNSGNNDLY NGKNNLYSGQNNVYSGIDPTSDNRGLTSGKHDSYSGIDLINDTLSGNQHIDIYDEVLK surface protein complement (join (52002. .53297,54200. .63307)) complement (join (52002. .53297, 54200. .63307)) /protein_id="CAD49095.1" /db_xref="GI:23498128" /db_xref="UniProt/TrEMBL:081219" /translation="MKIHYINILLFELPLNILIYNQRNHKSTNLHTQNNRSLCECELY 3.4e-65, 53.6% id in 375 /note="VAR exon II, could be alternate exon I upstream VAR gene PFD0005w" complement (join(48479. .49537,49768. .49821)) RKENELFGTNHVKHTTINRFAKPARDDPLHNQLELFHTWLDRHRNMCEKWNNKEELLD /codon_start=1
/product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_ide"CADB9096.1"
/db_xref="GI:23498129" /note="Similar to Plasmodium falciparum variant-specific surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 a note="synonym: /codon_start=1 /product="RIFIN" /note="synonym: PFD0015c" complement(join(48479. .49537,49768. .49821)) EDDIYYDVNDHDTSTVDSNTMDVPSKVQIEMDVNTKLVKEKYPIADVWDI" XLKEEWENETHSGNTHPSDSNKTLNTDVSIQIDMDNPKPINQFTNMDINVDTPTMDNM gene="RIF" gene="PFD0010w" gene="PFD0010w" Bcores: .46601 .46601 E(): 6.2e-103, 43.31% id in 3551 aa" PFD0020c" could be alternate exon II for (370 aa) fasta scores: E():

gene

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/db_xeef="Goa.gal118"

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Best Local Sim
Matches 275;
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                                                                                                                                                                                                                                            335664
                                                                                                                                                                                                        504 AAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAA 563
684 CTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAAGTCATTTTTATA 743
                                                                                                                                                                                                                                                                           444 CAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAATGTTTA 503
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                          AATATTATCCTATGATAATAAAGCTATTGTGGAAAATTATATTTTATGGAAAATATAATAT 335545
                                                                  CGTTCAGATTTTTCTTTTCATTCTTGTTATTTTTGTTATTTTTATATACATTTTCTT 683
                                                                                                     ATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGA 623
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                            5.4%;
                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                           Score 70.4; DB 3; Length 3; Pred. No. 0.00055; O; Mismatches 341; Indels
                                                                                                                                                                                                                                                                                                                                              Length 347582;
                                                                                                                                                                                                                                                                                                               0,
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7675 from Patent CQ422641 CQ422641.1 GI:41374870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lillie, J., Xu, Y., Wang, Y. and Steinmann, K. Novel genes, compositions, kits, and metho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   TTATTGTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                      AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTTCTTTTTCATTCTTTGTTATTTTG 658
                                                                                              TTAAANNTTTTNTAANTTATTAAACCAAAATTTTTTTTTAAAAAAATTTTTTAAAAANTT
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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PCR amplification of genomic DNA
Tomnlate: 50 ng
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit
                                                                                                                                                                                                                                                                          Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgatt@uci.edu
Primer A: TTCTACGTCCAAATGCATCAAAGA
Primer B: AGGAACCAAGCCTTATGAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopgida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 241)
MCMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
                                              Buffer:
Genomic DNA amplification
                                                                                         Amplicon sequencing
ABI protocol - using d-Rhodamine terminator
sequencing ready reaction with ampliTaq DNA;
Sequence ran on ABI 3700 sequencer.
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BV119878
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PZA01377 CML247
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STS size: 241
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                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brandon S. Gaut
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2003)
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/culfivar="CML247"
/db_xref="thaxon:4577"
/clone_lib="Zea mays CML247"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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/mol_type="genomic D
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20	c 19	c 18	c 17	c 16	c 15	14		c 12	c 11	10	9	ი 8	c 7	6	S	4	ω	2	۲	NO.	Result	
63.8	64	64.4	64.6	65.6	65.6	66.2	66.4	66.4	66.4	67.2	69.8	70.2	70.2	146	160.6	1311	1311	1311	1311	Score		
4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.3	5.4	5.4	11.1	12.3	100.0	100.0	100.0	100.0	Match Length	Query	•
431	9056	9859	9859	8056	346	439	6027	6027	6027	2657	13400	960	883	158	255	1394	1394	1394	1394			
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ABX44556	ABZ10100	ADS89440	ADS89714	ABZ10246	AAI87279	ABX35844	ADK12106	ABX09935	AAX58751	AAZ10551	ADR04296	ACN85231	AAL15210	AAH76334	AAH76340	AAH76333	AAH76332	AAX07409	AAX07408	ID		SUMMARIES
Abx44556 Bovine ES	Abz10100 Haematopo	Ads89440 Oligonucl	Ads89714 Oligonucl	Abz10246 Haematopo	Aai87279 Human pol	Abx35844 Bovine ES	Adk12106 cDNA enco	Abx09935 DNA encod	Aax58751 Maize dul	Aazl0551 DNA seque	Adr04296 Corn FT h	Acn85231 Breast ca	Aal15210 Human bre		Z. mays	.7	Aah76332 Z. mays M	Aax07409 Zea mays	Aax07408 Zea mays	Description		

The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably M845), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile

and infertile plants

New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.

Claim 2; Page 22-23; 39pp; English.

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58.6	58.6	58.8	59	59	59.2	59.2	59.4	59.4	60.2	60.2	60.4	60.4	60.6	60.6	61.4	62.4	63	63.4	63.4	63.4	63.4	63.4	63.6	63.6
	4.	5	4.5	4.5	5	5	4.5	4.5	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.8	4.8	4.8		4.8	4.8	4.8		4.9
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			Abl32871 Human imm	Acn56273 Cotton an	Abl70528 Chemicall	Abk31213 Signal tr	Aas46506 Tumour su	Adl43834 Human ova	Abn80326 Human che	Aas46636 Tumour su	Adl38222 Human ova		Abl33097 Human imm	Acn56344 Cotton an	Abl32909 Human imm	Ab192322 Chemicall	Abl34113 Human imm	Abn80285 Human che	Abk28424 DNA trans	Abl34085 Human imm	Aas46779 Tumour su	Aas45494 Chemicall	Aai61372 Soybean 2	Aai61371 Soybean 2

ALIGNMENTS

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RESULT 1
AAX07408
Ms45; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; maize; hybrid seed; fertility; ss.
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                                                                                                         WPI; 1999-105628/09.
                                                                                                                      Albertsen MC,
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                                   TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG
                                                TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT
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                                                  The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably M845), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encod - useful in mediating
     Sequence
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Matches 1311
                                                                                                                                                                   The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M845; male tissue;
hybrid seed; ds.
                                                                                                                  Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 46; 50pp; English.
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    mays Ms45 male tissue-preferred regulatory region

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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1311; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A male tissue-preferred regulatory region comprising nucleotide essential for initiating transcription of the MS45 gene useful f mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1394
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Best Local Similarity
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 Z. mays Ms45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 158 BP; 41 A; 50 C; 21 G; 46 T;
                  Homo sapiens
                                             Human; breast
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                                                                                                                                                             AAL15210 standard; cDNA; 883
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                                                                                                                                                                                                                                                               1274
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157; Conserv
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                                                                                                                                                                                                                                    GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                                                                               GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                                                                                                                                                            CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                                                                                    CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGGTTCGTC-TTGTTCCATCGTC
                                                                                                                                                                                                                                                                                             CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                                                                   CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTTGTTCCATCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                        cancer expressed polynucleotide 7667.
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                                                                                                     (first
                                           cancer; cell marker; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory region; transcription; male fertility;
                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%;
99.4%;
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                                                                                                                                                             BP
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Pred. No. 1.
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.5e-21;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 237;
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15-MAY-2000;
09-JUN-2000;
25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-2000; 2000US-0176077P
14-MAR-2000; 2000US-0189167P
24-MAR-2000; 2000US-0192099P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide useful as a marker for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides are also useful for isolating compounds with cytostatic activity
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                                                                                                                                                                                                                                                                                                                                                  AACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACA
GTTGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATT
                              AAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAA
                                                                                                                                                                                                                          TTATTGTTTTTATATACATTTTCTTCTCTCTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                                                                                                                                                                                                                               AATAANTTNAATTTTTTTAATNAAAAAAAAAATTTNAAATTTTAANCAANTNTTTTTT
                                                                                                                                                                                                                                                                                    AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTG
                                                                                                                                                                                                                                                                                                                                                                             CTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAAACCACGATCCTCTTAAAA
                                                       ТТТТСАЛАЛАЛАТТАGТТТАТТТСТСТТТАТАЛАЛАТАGAAAACACTTAGAAAAATAGA 898
                                                                                       AAAAAAATTTTTTNAAANTNTTTTTAAAACCTTNAATTNAAANANAATTTTTTTNNNTT
                                                                                                                 AAAAAAANNTTTTTTTTTTTTATANTTTATAAAAAATTTTATTTNTNTTTTTCTNAAAANA
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; 2000US-0193480P.
; 2000US-0205230P.
; 2000US-0211315P.
; 2000US-0220534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 322 A; 18 C; 23 G; 396 T; 0 U;
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Pred. No. 3.
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958

838 514 778 574 718 634

454

694 598 754 538 814

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RESULT 8
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                                                                                                                                                                                                             Query Match
Best Local S
Matches 237
                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide associated with breast detecting presence of polypeptide in sample, as a
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                                                                                                                                                                                                                                                                                                                                                                      at seqdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                                                                                                                                                                   237;
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                                                                                                                                                                                                                                         Similarity
TANAAATTTTTTNAAAAACTAATTNTAANNATANTNAATTTTTTNTAAAAAAANNNAAAAA
                                                                                                                                                                                                                                                                                                                       960 BP; 340
                                                    CTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAA
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                                                                                                                                                                                                                                   5.4*;
39.2*;
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New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 homologs, useful for floral development, e.g. engineering plant fi
                                                                                                                                                                                                                                                                                                       flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds.
                                                        WPI; 2004-580996/56.
                                                                                  Danilevskaya O, Hermon
Rafalski JA, Sakai H,
                                                                                                                                                                   30-JAN-2003; 2003US-00343477
                                                                                                                                                                                                                         12-AUG-2004
                                                                                                                                                                                                                                                   WO2004067723-A2
                                                                                                                                                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                         Corn FT homologue nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR04296 standard; DNA; 13400
                                                                                                                                                                                             29-JAN-2004; 2004WO-US002422
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DU PONT
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                          HI-BRED INT INC.
DE NEMOURS & CO
                                                                                   P, Bruggemann E, Cahoon
                                                                                                                           因 I.
                                                                                  Shirbroun D, R, Klein T;
                                                                                                                                                                                                                                                                                                                                                                          NO:63
                                                                                                Ananiev
  flowering
                  (Ap3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated polynucleotide comprising a CC first, second, third, fourth or fifth nucleotide sequence, or their CC complement encoding a polypeptide either having flowering locus T gene CC (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also CC composenting a cell with the polynucleotide; (3) transforming a cell by transforming a cell with the polynucleotide; (3) transforming a cell by CC transforming a cell with the polynucleotide; (4) a cell comprising the CC recombinant DNA construct; (5) producing a plant comprising transforming to a plant cell; (6) a plant comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (7) a seed comprising a first nucleotide sequence contains at least 30 nucleotides, and where the CC first nucleotide sequence is comprised by another polynucleotide, where the other polynucleotide includes the second, third, fourth, fifth or CC sixth nucleotide sequence; (9) an isolated polypeptide having FT or Ap3 CC encoded by the polynucleotide comprising isolating the polypucleotide comprising isolating a polypeptide containing a recombinant DNA construct comprising the polypucleotide from a cell containing a recombinant DNA construct comprising the polypucleotide coperably linked to a regulatory sequence. The polynucleotides are useful for floral development, e.g. engineering plant sterility/fertility, cc flowering time, plant growth rate of cell division to enhance cc culcure morphology and the rate of cell division to enhance construct comprise and plant sterility enhances are useful concleotide sequence from the present sequence represents an FT homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                        P-Ztap promoter; male sterile plant; glyphosate tolerance; male reproductive tissue; hybrid seed production; crop out; flower life; ss.
                                                                                                                                                                                                                                                                                                                                                                                                    AAZ10551 standard; DNA; 2657 BP
                                                                                                                                                                                                                                                                                 DNA sequence of the P-Ztap promoter of maize.
                                                                                                                                                                                                                                                                                                                                                              AAZ10551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;
                 09-MAR-1998;
                                                     09-MAR-1999;
                                                                                           16-SEP-1999
                                                                                                                              WO9946396-A2
                                                                                                                                                                  Zea mays
                                                                                                                                                                                                                                                                                                                           16-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                       (first entry)
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                 98US-0077277P
                                                       99WO-US005126
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73.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.8;
Pred. No. 8e
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. 8e-05;
32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13400
                                                                                                                                                                                                                                           glyphosate;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC the production of male sterile plants. The method comprises selective coparably linked to a separate promoter, whereby the first promoter causes tolerance to glyphosate. The method uses two DNA molecules, each coparably linked to a separate promoter, whereby the first promoter copyphosate, and the second promoter functions in plant cells to produce a protein that causes tolerance to glyphosate, and the second promoter functions in plant cells to cause the production of a second RNA sequence in a male reproductive tissue.

CC Expression of the DNA promotes tolerance to glyphosate in those tissues in which it is expressed. Expression of the second DNA molecule causes the production of an RNA sequence which can inhibit the glyphosate couses the production of an RNA sequence which can inhibit the glyphosate copyphosate tolerance generated by expression of the first DNA molecule. By using a component for the second DNA molecule which restricts the production of the antisense RNA to only a subset of the tissues which express the first CNA molecule, only the subset of the sissues which express the first CNA molecule, only the subset of the tissues which express the first CNA molecule, only the subset of tissues in which the second DNA molecule is expressed will be susceptible to glyphosate toxicity. In this way, a component of the plants for use in the production of the producting upon the component of the plants for use in the production of hybrid seed, for minimizing cundesirable crop outcrossing, and for lengthening flower life. The methods can be used wit h plants such as corn, wheat, rice, canola, oat, barley, alfalfa, carrot, cotton, oilseed, oilseed rape, sugarbeet, cotton, oilseed, oilseed rape, sugarbeet, conditions to continue and squash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
               misc_feature
                                                                                  Zea mays
                                                                                                                      Starch synthase; SSII; DU1; dull1 gene; maize; transgenic plant; ss.
                                                                                                                                                              Maize dull1 gene encoding starch synthase enzyme DU1
                                                                                                                                                                                                             16-AUG-1999
                                                                                                                                                                                                                                                       AAX58751;
                                                                                                                                                                                                                                                                                                  AAX58751 standard; cDNA; 6027 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2657 BP; 686 A; 611 C; 677 G; 683 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1A-B; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of male sterile plants using a gene encoding glyphosate tolerance, used for, e.g. production of hybrid seed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the P-Ztap promoter of maize. It is unin the method of the invention. The specification describes a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MONS ) MONSANTO CO
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                                                                                                                                                                                                                                                                                                                                                                                                           2002
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                                                                                                                                                                                                                                                                                                                                                                                                      ACTAGCCCTAAA 2013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTAGCCCTAGA 918
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                                                                                                                                                                                                           (first entry
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                 Location/Qualifiers
1. .1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.1%;
74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67.2;
Pred. No. 0.
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CC illustrate the role of the dul locus in starch biosynthesis, a transposon CC tagging strategy was used to isolate the gene and describe its collection reports tagging of the dul locus with CC polypoptide product. The invention reports tagging of the dul locus with CC mutransposon, cloning and characterisation of a portion of the gene, and sequence (see AAY06199) deduced from this cDNA indicates that Dul codes CC for a 186 kDa protein extremely similar to potato tuber starch synthase CC endosperm. The Dul product contains unique sequence features in its N-cc multiple aspects of starch biosynthetic enzymes. Mutations within the maize SIII gene affect CC multiple aspects of starch biosynthase(s), starch branching enzyme(s) and possibly starch debranching enzyme(s). The isolated cDNA can be used to provide an cc enzyme with which to regulate the production of starch, and with which to produce altered or novel forms of starch, e.g. in transgenic plants. CC Expression of Dul in bacteria and yeasts also modifies glycogen it that code for functional portions of DUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of the maize gene dull1 (du1). illustrate the role of the du1 locus in starch biosynthesis, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 104-107; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in Claim 14"
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/note= "functional
in Claim 17"
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in Claim 18"
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'note= "functional fragment of cDNA specifically claimed
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Query Match Best Local Similarity

5.1%; 77.5%;

Score 66.4; Pred. No. 0

DB 2; 1609

Length 6027;

Sequence

6027 B₽,

1800 A;

1177

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Query Match Best Local S Matches 93

Similarity

5.1**%**; 77.5**%**;

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Other

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RESULT 12
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                          improved affinity to starch and modified catalytic capabilities and to the in vivo and in vitro synthesis of glucan chains of modified lengths as compared to plants producing native starch or starch produced with native starch synthases. Expression of the starch synthase fusion proteins along with granule bound starch synthase (GBSS) will lead to a modified starch having an altered or improved morphology, retrogradation, waterbinding, or swelling potential of the granules, gel strength, adhesiveness, cohesiveness, hardness, elasticity, increased or decreased granule size, degree of branching, crystallinity, degree of cross-linking, and increased or decreased glucan chain lengths. This sequence encodes a starch synthase used in the invention
                                                                                                                                                                                                                 protein consisting of 4 different functional domains selected from glucan association domain (GLASS), linker domain (LINKR), glucosyl transferase domain (GTYTR), and C-terminal end (CTEND) which are operably linked to one another. The DNA molecule is useful for expressing in plants polypeptides including starch synthase enzymes as fusion proteins with
                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding fusion protein consisting of 4 different functional domains selected from glucan association domain, linker domain, gluce transferase domain, and C-terminal end, useful for producing modifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granule bound starch synthase; GBSS; morphology; retrogradation; waterbinding; swelling potential; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Starch; starch synthase; glucan association domain; GLASS; linker domain; LINKE; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
                                                                                                                                                                                                                                                                                                                                           Claim 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commuri P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001;
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                                                                                                                                                                                                                                                                                                          The invention describes an isolated DNA molecule encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-040678/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2002
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                                                                                                                                                                                                                                                                                                                                          Page 225-227; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                           Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of a maize gene, dull 1 (DUI), and the polypeptide it encodes. The DUI polypeptide has starch synthase activity, and comprises an N-terminal arm region, a C-terminal catalytic region, and a region of about 900 amino acids terminating with the catalytic region. The C-terminal catalytic region has a catalytic domain comprising alpha-1,4-glycosyltransferase catalytic activity. The dull polymucleotide sequence is useful in producing starch e.g. from a
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid designated dull1, encoding a starch synthase, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004049810-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
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12-MAY-2000; 2000US-00554467
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                                                                                                                                                                                       Similarity
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                                                    TCTACGGGCTAGTTTGGGAACCCCATTT-TTCCAAGGGATTTCCATTTTTCCAAGAAAA
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                                                                                                                                                                                                                                                                                                                                             plant or transfected cell. The present
                                                                                                                                                              Conservative
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120. .5144
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77.5%;
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                                                                                                                                                         Score 66.4; DB 12;
Pred. No. 0.00035;
0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                             sequence encodes maize
                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                  Other
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RESULT 14
ABX35844
ID ABX35
CC of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and CC (2) determining a level or pattern of a molecule in a bovine cell or CC tissue comprising: (a) incubating a marker nucleic acid (comprising any CC of the 15112 nucleic acid sequences or its complement or fragment) with a CC complementary nucleic acid molecule obtained from the bovine cell or CC tissue, where hybridisation between the marker nucleic acid and the CC complementary nucleic acid molecule obtained from the bovine cell or CC detecting the level or pattern of the complementary nucleic acid, where CC level or pattern of the molecule; and is used for CC determining a level or pattern of a molecule; acid is used for CC it is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or CC it is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or CC isometric texpressed sequence is one of the CC isometric sequence was not shown in the specification but was obtained in CC electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                               lactation or muscle and fat deposition (designated LMPD), derived from cattle, and the LMPD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMPD nucleic acid linked to a promoter and a 3, non-translated sequence that functions in the cell to cause termination of transcription and addition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                     seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 1009; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Byatt JC, Mathialagan
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(TAON/)
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11-JAN-2000; 2000US-00480902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BYATT J C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with lactation/muscle/fat deposition
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Best Local Similarity
Matches 134; Conserv
The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines or other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or eptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemacpoiesis regulating activity, tissue growth factor activity, hamboropoiesis regulating activity itseue growth factor activity, immunomodulatory activity and activity inhibbin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                             Isolated
                                                                                                                                                                                                                                                                           WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
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                                                                                                                                                                             SEQ
                                                                                                                                                                                                         nucleic acids and polypeptides, useful for ting e.g. leukemia, inflammation and immune
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llarity 54.3%;
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Best Local :
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                                                                                                                                                                                                                                                                                                             Sequence 346 BP; 188
                        989
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94
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 TTTTTTTTTTTTTTTTTTTCTTTTTTT
                 CTTACAATAGAGTGATTTTCTTCCGATTTTAT 717
                                                 TATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGACG
                                                                                                                                                                              GAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAAAT
                                                                           TTCAGATTTTTCTTTTCATTCTTGTTATTTGTTATTGTTTTTATATACATTTTCTTCT
                                                                                                   GACTTATATATATATATAAATTTTTTTTTTTAGAAAATAATTTACATTTAAACAATAAAA
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63
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Search completed: September 15, 2005, 21:33:05 Job time: 636.708 secs

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Sequence 17600, A Sequence 16997, A Sequence 15635, Sequence 22, Appl Sequence 1280, Ap Sequence 14876, Ap Sequence 14164, A

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1280, Ap 14164, A 14164, A 2813, Appli 2813, Ap 16001, A 1, Appli 16110, Appli 16110, A 11934, A 11, Appli 11, Appli

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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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1311
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  US-08-880-499-1
US-08-968-542C-1
US-08-968-542C-1
US-09-954-467A-1
US-08-487-826B-13
US-09-902-540-1357
US-09-902-540-1357
US-09-906-499-2
US-09-806-708B-23
US-09-806-708B-23
US-09-640-173-53
US-09-713-550-53
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Sequence 15349, A
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Sequence 15307, A
Sequence 15307, A
Sequence 15309, A
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                                                                                                                    ; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: [
US-08-880-499-1
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US-08-880-499-1
; Sequence 1, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; The second of the s
                                                                                                                                                                                                        TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STERNBERNESS: 1321
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                      Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
SOFTWARE: PatentIn Release #1.0, Vers
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricla 7.3
REGISTRATION NUMBER: 32,73
REGERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
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APPLICANT: 1
APPLICANT: 1
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ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave.,
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
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APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
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APPLICANT:
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Carl, Garnaat W.
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RESULT 2
US-08-880-499-2
US-08-880-499-2
Sequence 2, Application US/08880499
Sequence 2, Application US/08880499
Patent No. 6037523
Patent No. 6037523
Patent No. 6037523
APPLICANT: Fox, Tim W.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: AMALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AMD METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genom
US-08-880-499-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENTATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 1311; Conserv
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Darwin Building, 7100 N.W. 62nd Ave., P.O.
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Pred. No. 1.1e-313;
0; Mismatches 0;
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US-08-968-542C-1
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                                                                                                                         Query Match
Best Local
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                                                                                                              Matches
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APPLICANT: Myers, et al.
TITLE OF INVENTION: dull1 Coc
TITLE OF INVENTION: Synthase
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                            ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: maize
TISSUE TYPE: endosperm
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (713) 777-232
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, P
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D603
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: No. 5981
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
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HYPOTHETICAL:
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TX
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                                                               CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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Pred. No. 2.4e-06;
0; Mismatches 26;
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SEQ ID NO 1
LENGTH: 6027
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08410784A Patent No. 5912413
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESIQ VEGRION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,7:
FILING DATE: 24-MAR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/554,467A
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/US98/24225
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 08/062,102
PRIOR FILING DATE: 1997-11-12
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APPLICANT: James, Martha G.
TITLE OF INVENTION: dull1 Coding for a No.
TITLE OF INVENTION: Thereof
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MYERS, ALAN M.
APPLICANT: JAMES, MARTHA G.
APPLICANT: JAMES, MARTHA G.
TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING
TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE
TITLE OF INVENTION: SUGARY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: cDNA sequence corresponding OTHER INFORMATION: starch synthase enzyme DU1.
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                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             STREET: 10. Boston
                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02109
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                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Weingarten,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5606 TCTACGGGCTAGTTTGGGAACCCCATTT-TTCCAAGGGATTTCCATTTTTCCAAGAAAAA
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93; Conserv
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Ten Post Office Square
                                                                                                                                                                                                                                                                                        USA
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77.5%;
                                                                                                                       US/08/410,784A
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Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6639125el Starch Synthase and Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08487826B Patent No. 5993827
         ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B

FILING DATE: 10-SEP-193

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: ISTREISED, Ned

REGISTRATION UNUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Sim, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Heine, Ph.D., Holliday C
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: ISU-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-451-0313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Peterson, David S. Su, Xin-zhaun Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sim, Kim L.
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Pred. No. 0.00015;
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                                                                                                                                                                              #1.25
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
TYPE: nucleic acid

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CURRENT FILING DATE: 1999-05-14
NUMBER OF SCO ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 5397
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5397, Applia Patent No. 6476212 GENERAL INFORMATION:
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Best Local Similarity 50.2%;
Matches 141, Conservative
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                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700350078H1
NAME/KEY: unsure
LOCATION: 10, 12, 185-186, 204, 253, 274, 278
OTHER INFORMATION: 8, t, c, g, or other
                                                                                                                                                                                                                                                                      ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                             Local Similarity 69.0
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AAATTAGTTTATTTTCTCTTTAT-AAAATAGAAAACACTTTAGAAAAATAGAGTTGCCAGA
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                                                                               TTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAA 848
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                                                                                                             Score 55.8; DB 4;
Pred. No. 0.00031;
0; Mismatches 39;
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Pred. No. 0.00078;
0; Mismatches 140; Indels
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                                                                                                                                          Length 279;
                                                                                                              Indels
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                                                                                                             Gaps
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RESULT 9
US-08-880-499-1/c
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; LICATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
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US-09-902-540-1357/c
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genom
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                  Sequence 1, Application US/08880499
Patent No. 6037523
GENERAL INFORMATION:
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Fox, Tim W.
APPLICANT: Garl, Garnaat W.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
LENGTH: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Myxococcus xanthus
FEATURE:
                    CORRESPONDENCE ADDRESS
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440
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                                                                                                                                                                                                                                                                                                                                320 TATTTTA 314
                                                                                                                                                                                                                                                                                                                                                                       866 CTTTATA 872
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAGCCCTA 131
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
PIONEER HI-BRED INTERNATIONAL, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%;
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Pred. No. 0.00047;
0; Mismatches 120
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                                                                                                                                                                                                                            ; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertsc
APPLICANT: Fox, Tin
APPLICANT: Carl, Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4804
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: Bingle
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08880499
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLODS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
CLASSIFICATION: 800
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MOLECULE TYPE:
                                                                                                                                                         APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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STREET: Box 100
CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
                                      STATE:
                                                                    STREET: Darwin B
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                  COUNTRY:
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50131
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                  Iowa
7: USA
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                                                                                     Darwin Building,
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                                                                                     PIONEER HI-BRED INTERNATIONAL, INC
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Pred. No. 0.00064;
0; Mismatches 84;
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                                                                                    US-09-806-708B-23
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                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 23
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TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
CHARACTERISTICS:
  Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-59741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEG ID NOS: 23
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Application US/09806708B Patent No. 6784342
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                                                                                                   FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1059
OTHER INFORMATION: (
                                                                                                                                                                              LENGTH: 1055
TYPE: DNA
ORGANISM: Artificial sequence
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION: NAME: Sweeney, Patricia REGISTRATION NUMBER: 32,
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REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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Local Similarity 55.8%;
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                                                                                                     consensus sequence of A.t. and L.a. FAEl promoters
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      430;
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                                         Length 1055;
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      Indels
    15;
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Sequence 1, Application US/09004056A
Patent No. 6566586
GENERAL INFORMATION:
APPLICANT: Calgene LLC
TITLE OF INVENTION: Plant Expansin Promoter Sec
FILE REFERENCE: 125
CURRENT APPLICATION NUMBER: US/09/004,056A
CURRENT FILING DATE: 1998-01-07
FARLIER APPLICATION UNMBER: 60034914
EARLIER APPLICATION UNMBER: 60034914
EARLIER FILING DATE: 1997-07-01
WIMBER OF SEQ ID NOS: 1
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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US-09-004-056-1/c
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SEQ ID NO 53
LENGTH: 396
                                                         Query Match
Best Local Similarity
Matches 139; Conserv
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: OTHEREFOR TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
NUMBER OF SEQ ID NOS: 196
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Best Local Similarity
                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or
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OTHER INFORMATION: unknown
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                    TTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTATATACATTTTCTTCTTCTTACA 691
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Pred. No. 0.00056,
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVI
FILE REFERENCE: 210121.484C4
CURRENT APPLICATION NUMBER: US/09/713,550
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 205
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
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GENERAL INFORMATION:
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Best Local Similarity 43.8%;
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NAME/KEY: misc feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C
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NTNNTTNNNNNANNGGG
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Pred. No. 0.00056;
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APPLICANT: XX, Jiangchun
APPLICANT: XX, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 21011.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYDEN DANS
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Search completed: September 15, Job time: 200.304 secs
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US-09-825-294-53
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Best Local Similarity
Matches 139; Conservat
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Patent No. 6710170
GENERAL INFORMATION:
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Pred. No. 0.00056;
0; Mismatches 178;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

							No. Score	Result	
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ALIGNMENTS

RESULT 1 US-10-713-381-1

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; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-1
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Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMYY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
BEST TATION NUMBER: C0/802 400
                                                                                                                                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1394
  Query Match
Best Local Similarity
Matches 1311; Conserv
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
    Conservative
100.0%; Score 1311; DB 20; 100.0%; Pred. No. 5e-275; ative 0; Mismatches 0;
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Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1311; DB 20; Best Local Similarity 100.0%; Pred. No. 5e-275; Matches 1311; Conservative 0; Mismatches 0;
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Sequence 9, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GRANAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMOY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
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US-10-713-381-3
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 158
TYPE: DNA
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Best Local Similarity
Matches 157; Conserv
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Best Local Similarity
Matches 163; Conserv
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LENGTH: 255
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUS-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SCO. IN NOS. 24
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Zea mays
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Gac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 23340
LENGTH: 320
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                                                                                                                                              Query Match
Best Local Similarity
Matches 95; Conserv
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Best Local (
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LENGTH: 1261
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                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: LIB3595-039-G8_FLI
                                                                                                                                                                                                                                                                   FEATURE:
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851 ATTAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTA
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                                                                                                  791 TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAAAA 850
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                                                                                                                                              Conservative
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                                                                                                                                          Score 74; DB 18; Length 320; Pred. No. 4.8e-06; Mismatches 35; Indels
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Pred. No. 3.1e-07;
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; OTHER INFORMATION: US-10-425-115-141826
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APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16264
LENGTH: 624
TYPE: DNA
COCCNETANT FILING
                                                                                                                                                       FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 141826
LENGTH: 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity 73.1%;
  Query Match
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAAAA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTTAATT 503
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                                                                    Clone
                                                                    ID:
                                                               MRT4577_60829C.1
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Pred. No. 6.7e-06;
0; Mismatches 39
  Score 73;
  DB 20;
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Length 1326;
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RESULT 10
US-10-425-115-83293/c
US-10-425-115-83293/c
Sequence 83293, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: Lo Rosa, Thomas J.
APPLICANT: Kovallo, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT FILMS DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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US-10-425-114-32493
Sequence 32493, Application US/10425114
Publication No. US20040034888A1
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32493
LENGTH: 2445
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Best Local :
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTAGTTTATTTTCTCTTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGTTGCCAGACTA 910
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Kovalic, David K.
Screen, Steven E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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73.6%;
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Pred. No. 2.3e-05;
0; Mismatches 37;
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); Mismatches 50;
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SEQ ID NO 51470
LENGTH: 1203
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1203)
OTHER INFORMATION: unsure at a.
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                                                                                                                                                                                                                                                                                                                                                          US-10-425-115-51470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51470, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Best
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Best Local Similarity 60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21 (5322) B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2729)
OTHER INFORMATION: unsure at
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OTHER INFORMATION: Clone ID: MRT4577_146936C.1
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                                                                                                                                                AAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAG
                                                                                                                                                                                                    ACTITATIAAGGGCTAGTGGGGGAA-CATATTTTCCAAAAAGATTTCTATTTTCTTAAA
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76.1%;
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Pred. No. 2e-05;
0; Mismatches 31;
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Pred. No. 2.
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ACTAGCTCTAAGAT 1057

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US-10-425-115-142853/c
; Sequence 142853, Application US/10425115
; Publication On US20040214272A1
; GENERAL IMFORMATION:
; APPLICANT: La ROBA, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and
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                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_61761C.1 US-10-425-115-142853
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                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 142853
LENGTH: 1123
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17816
LENGTH: 928
LENGTH: 928
     Matches
                                        Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                              FILE REFERENCE: 38-21 (53222) B
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ORGANISM: Zea maye
                                                                                                               ORGANISM: Zea mays FEATURE:
                                                                                                                                                      TYPE: DNA
                       Local
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                       Similarity
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                       78.0%;
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Score 71.8; DB 20;
Pred. No. 2.7e-05;
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Pred. No. 2.4e-05;
0; Mismatches 27;
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                                    Length 1123;
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US-10-425-115-52216
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US-10-425-114-31957
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cap, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILD REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER D. SEC IT NOC. 27128
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 52216
LENGTH: 2537
                                                                                                                                                                                                     Sequence 52216, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31957
LENGTH: 2537
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                                                        TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                         APPLICANT: Kovalic, Dav
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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OTHER INFORMATION: Clone ID: UC-ZMFLB73238H12_FLI
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73.4%;
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Pred. No. 3.9e-05;
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                                                                                                                                              and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                           Database :
                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

Qу 4 Db	Query Match Best Local Matches 90	ORIGIN	FEATURES BOUTCE	AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 CC656933 LOCUS
04 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCCAGAACAAGATTTAAAAAAAA	Query Match 69.3%; Score 908; DB 9; Length 963; Best Local Similarity 100.0%; Pred. No. 7.8e-180; Matches 908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		TIGR P712 Medic Tel: 301-6 Fax: 301-6 Email: whi Seq primer Class: she	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Praser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002) Other_GSSs: OGWDQ20TV Contact: Cathy Whitelaw	OGWDQOTM ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence. CC656933.1 GI:32060225 CC656933.1 GI:32060225 GSS. Zea mays Zea mays Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	963 bp DNA

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Fax: 301-838-0208
Email: whitelaw@tigr.c
Seq primer: TF
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(bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Ro Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
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Other_GSSs: OG1AG08TH
Contact: Cathy Whitelaw
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CC656939 1 GI:32060231
GSS.
Zea mays
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterbac Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)
Other_GSSs: OGWDQ2OTM
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                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cathy Whitelaw
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            GTGCCTACGTCAGGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTT 1188
                                                                                                                                   AGTCATTGTCCCTGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAG
                                                                                                                                                                            TATAATTATTTGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                          /clone="ZMMBMa0554D15"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0."
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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Pred. No. 1.6e-77;
0; Mismatches 2;
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one ZMMBMa0554D15,
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Best Local Sim
Matches 125;
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                                                                                                                                                                                                                                                      135 TCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCATCTGACCGAGGCCCA 194
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OG48B05FC ZM 0.7 1.5 KB Z

genomic survey sequence.
CG252571

CG252571.1 GI:34154661
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(bases 1 to 715)

whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)

Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: whitelaw@tigr.org
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic_DNA library"
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="Laxon:4577"
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80.1%; Pred. No. 1.2e-09;
vative 0; Mismatches 30
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DEFINITION

CL235046 967 bp ZMMBBb0575001r ZMMBBb (HindIII)

Zea mays genomic clone

DNA

linear

GSS 15-JAN-2004

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KEYWORDS
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Best Local Similarity
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                TITLE
                                                              AUTHORS
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PUILO19TB ZM 0.6 1.0 KB Z
genomic survey sequence.
CG048704
CG048704.1 GI:33920884
GSS.
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CL235046
CL235046.1 GI:4089
GSS.
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Zea mays
                                       1 (bases 1 to 814)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messi Sequencing of the maize genome at PGIR (2003c)
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Class: BAC ends
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The Plant Genome Initiative at Rutgers, Waksman Institute,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Clade; Panicoideae; Andropogoneae; Zea.
Unpublished
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                               Bennetzen, J
                                                                                                                                           Zea mays
                                                                                                                                                          Zea mayв
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Contact: Bharti, A.K.
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Location/Qualifiers
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732 445 5735
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                Genomics Consortium
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/note="Vector: pCUGI; Site_1: HindIII; Site_2:
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/cultivar="B73"
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lab_host="E. coli DH10B"
clone_lib="ZMMBBb (HindIII)"
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78.6%;
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(2003)
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Pred. No. 8.5e
0; Mismatches
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Zea mays
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                                                                                                                    Sequencing of the maize Unpublished (2003) Contact: Rod Wing
                                                                    Arizona Genomics Institute
University of Arizona
Biological Sciences West,
                                                                                                                                                                                                                                                                                                               genomic survey sequence.
CG414922
CG414922.1 GI:34505144
           Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                   Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 754)
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Contact: Cathy Whitelaw
TIGR
                                                                                                                                                                       and Wing, R.
                                                                                                                                                                                     Yu, Y., Kim, H.R.,
                                                                                                                                                                                                                                                                  Zea mays
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Tel: 301-838-5843
                                                            85721-0088, USA
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/clone=11b="ZM 0.6 1.0 KB"
/clone=1vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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                                                                                                                                                                                     Hatfield, J.,
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Gaps

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ZMMBBb0290L09

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08-SEP-2003 0L09 3',

Tucson,

ΑZ

Messing, J

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AUTHORS
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                                                                                                                                                                                                                                  Contact:
                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                              PUHRV15TB ZM_0.6_1.0 KB Zea mays genomic clone genomic survey sequence.
CC439901
CC439901.1 GI:30940477
GSS.
                                                                                                                                                                                                   9712 Medical Center Drive,
Tel: 301-838-5843
                                                                                                                                                                                                                                                           Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHRV15TD
                                                                                                                                                                                                                                                                                                   Thus, Frager, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: M13r
Plate: 0290 row:
Seg primer: M13r
                                                                                                                                                                        Email: whitelaw@tigr.org
                                                                                                                                                                                       Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD:
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/cultivar="873"
/db xref="raxon:4577"
/clone="zMMBBb0290L09"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                            Cathy Whitelaw
/db_xref="taxon:4577"
/cloine="zMMBTa519D06"
/cloine_lib="ZM_0.6 1.0 KB"
/cloine="Vector: pCR4-TOFO; Site_1:
/note="Vector genomic DNA library"
                                                                     /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                             location/Qualifiers
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Pred. No. 6.4e-08;
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                ECORI;
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cone ZMMBTa519D06
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Best Local Similarity
Matches 131; Conserv
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Zea mays
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1 (bases 1 to 652)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUHOC67TB ZM 0.6 1.0 KB genomic survey sequence. CC384247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
Other_GSSs: PUHOC67TD
                                                                                                                                                                                                                                                                                                                                                                                                Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize Genomics Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAA 893
                                                                           ACTAGCCCTAAAGTATTTTATAAAATAGAGAAAAATTCGTCTATTTTTCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAAATTAGTTTATTTTCTCTTGAGAAAATATAAATCACTTGAGAAAATATAGTTTCCAA
                                                                                                                                                                     Conservative
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/clone lib="ZM_0.6_11.0 KB"
/notee="Vector: pCR4_TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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Pred. No. 1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
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RESULT 10
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Best Local S
Matches 163
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Andropoconeae; Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Praser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Other GSSs: PUHLU61TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC400575 797 bp DNA linear GSS 19-MPUHLU61TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa480L01,
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                         TTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTT
                                                             AATTATTTGGCCAGCCCCATAAATTATTTAAAC 984
                                                                                                               AAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTAT
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                                                                                                                                                                                            TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
                                      ATTTCAAATTCCACTTTGCAAAATAGTGTCATC
                                                                                        AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCGATAAATCCCCTATCTCATTCTCT
                                                                                                                                       TTCATTCTCACAAGGGAAAAATAGTTTATTTCCCTTTTGTAAAATGGTAATCACTCGGAA
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                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
/clone="zMMBTa480101"
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="genomic D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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59.7%;
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                                                                                                                                                                                                                                                                                               Score 86.6; DI
Pred. No. 1.1e.
0; Mismatches
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1.1e-07;
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Best Local S
Matches 163
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Local Similarity
PUJBE19TB ZM 0.6_1.0_KB Z
genomic survey sequence.
CG103452
CG103452.1 GI:33985746
GSS.
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PUHLU61TB ZM 0.6 1.0 KB Z
genomic survey sequence.
CC400574
CC400574.1 GI:30880664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD slade; Panicoideae; Andropogoneae; Zea. clab; Panicoideae; Andropogoneae; Zea. to 820)

1 (Dases 1 to 820)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2003)
Other_GSSs: PUHLU61TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: TR
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize Genomics Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
                                                                                                                                                                                                                                   ATTTCAAATTCCACTTTGCAAAATAGTGTCATC
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                                                                                                                                                                                                                                                                                                                   AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCGATAAATCCCCTATCTCATTCTCT
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/clone_lib="ZM_0.6_1.0_KB"
/clone_tib="ZM_0.6_1.0_KB"
/note="Westor: pCr44_TOPO; Site_1: EcoRI; 0.6-1.0
CoT_selected_genomic_DNA_library"
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/mol_type="genomic DNA"
/strain="B73"
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Pred. No. 1.1e-07;
0; Mismatches 109;
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genomic
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                                                                                                                                                                                                                                                                                         CG082135 765 bp DNA line PUFQX12TD ZM 0.6_1.0 KB Zea mays genomic clone genomic survey sequence.
CG082135
CG082135.1 GI:33964429
                                                               Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFQX12TB
Contact: Cathy Whitelaw
                                                                                                                                      1 (bases 1 to 765)
Whitelaw.C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUJBE19TD
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1 (Dases 1 to 471)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                  Tel:
                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                            Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: TR
 Medical Center Drive,
301-838-5843
301-838-0208
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/clone=11b="ZM 0.6-1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 85.4; DB 9;
Pred. No. 2e-07;
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                                   Rockville,
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                                 MD 20850, USA
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JOURNAL
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AUTHORS
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CC630219/c
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Best Local
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
Zea mays
                                                                                                                                                                                                                                                         9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey CC630219
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC630219.1
                                                                                                                                                                                                            Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                           Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: whitelaw@tigr.org
                                                                                                                                                                                                                                            Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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1. .765
                                                                                                                             /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                             organism="Zea mays"
                                                                                                                                                                           , .781
                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic
/strain="873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Zea mays"
                                                                                                                  db xref="taxon:4577"
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.58
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907 ACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTTG 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        787 AITITITAAGAGCTAGITTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 781)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUG53TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGUCGS3TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0406J09,
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/note="Vector: pBCSK-; Site 1: HincII; 0.
methylation filtered genomic DNA library"
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Pred. No. 2.2e-07;
0; Mismatches 48;
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Length 781;
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SOURCE
ORGANISM
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AUTHORS
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CG349565/c
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Best Local Sim
Matches 125;
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                                                                  847 AAAAATTAGTTTATTTTCTCTTTATAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAG 906
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 815)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Cleek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSe: OGOF183TV
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG349565 815 bp DNA linear GSS 26-AUG-2003 GOGFI83TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0705N21, genomic survey sequence.
CG349565
CG349565.1 GI:34266831
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: TR
Class: sheared ends.
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                         ACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG 960
                                                                                                                                                                         ATTITITAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAA 846
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                                                                                                                                                                                                           6.5%;
llarity 71.8%;
Conservative
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/clone lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK.; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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Pred. No. 2.2e
0; Mismatches
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0; Mismatches 48;
                                                                                                                                                                                                                           ; DB 9;
2.2e-07;
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                                                                                                                                                                                                                                           Length 815;
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Search completed: September 16, 2005, 08:08:18
Job time : 4089.83 secs

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Maximum DB
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Perfect score:
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887654321098765
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   1394
1311
1311
1311
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Match Length
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Gapop 60.0 , Gapext 60.0
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1394
1 ccatggtgtctctatgaaaa.....ctttttcgtccaccacgtg
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  100.0 1394

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94.0 1394

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94.0 1394

13.0 158

3.6 158

3.6 29

1.7 10384

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ALIGNMENTS

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 AX224395 á ş 밁 밁 밁 S ORIGIN FEATURES source FOCUS Query Match Best Local : Matches 1394; 181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 121 121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 13 Zea mays Zea mays 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 2 23-AUG-2001, PIONEER HI-BRED INTERNATIONAL, INC. (US) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. AX224395 1394 bp Sequence 2 from Patent WO0160997. AX224395 h 100.0%; Score 1394; Similarity 100.0%; Pred. No. 0; 94; Conservative 0; Mismatches AX224395.1 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGTGCATGAT /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" Mismatches DNA DB 6; 0, Indels Length 1394; linear and Kendall,T.L. of using same PAT 10-SEP-2001 0; 180 120 240 180 120 60

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01 TTATTATTCTTTAGATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 360 	41 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300 	21 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180 81 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	61 61 21	100.0%; Score 1394; DB 6; Length 1394; Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; hes 1394; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	BD062177 Male tissue-preferred regulatory region and method of using same. BD062177.1 GI:22607782 JP 2001520523-A/2. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Loses 1 to 1394) Albertsen, M.C., Fox.T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1394) Albertsen, M.C., Fox.T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L. Male tissue-preferred regulatory region and method of using same Patent: JP 2001520523-A 2 30-OCT-2001; PROUNEER HI BRED INTERNATIONAL INC DN JP 2001520523-A/2 DD 30-OCT-2001; PF 19-JUN-1999 JP 1999504910 PR 23-JUN-1999 JP 1999504910 PR 23-JUN-1997 US 08/880499 PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFWAN, PC (12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC COTKL4/34,C12Q1/68, PC A01H5/00 CC Strandedness: Single; FH Key Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Locationsem="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	381 CGTCCACCATG 1394 381 CGTCCACCATG 1394	1321 AAAGATCACAACAGCTAGCGTTCTCCCGCTAGCTTCCCCTCTCCTCCTGCCGATCTTTTT 1380

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		1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260	1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140	961 GCCAGCCCATAAATTATTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020	941 TTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAACACTTAGAAAAATAGAGT 900	661 ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720
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	481 CGAAGCTATCATGTAATGTTTAAAGAACATCTATTAAAACCACCATCCTCTTAAAAAAACATCAT	361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG	241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA	121 CTCCATGITCCACITCTCCCACCTCGCGITGCACATTTCTTGGATGTCGGTGGTTCCCAT	1 CCATGGTGTCTCTAIGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC	FH Key Location/Qualifiers. 1. 1394 1. 1394

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Fox.T.W., Trimmell,M.R. and Albertsen,M.

Direct Submission

Submitted (13-MAR-2001) Trait and Techno

Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave.,

IA 50131-1004, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF360356
Zea mays
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mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldae; Andropogoneae; Zea.
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x,T.W., Trimnell, M
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SRKDHLNILLEGEGTGRLLRYDPETSGVHVVLKGLVFPNGVQISEDHQFLLFSETTNC
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TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG TTCAAAAAAATTAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGT ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTTACAAACATCTAAGAGCGACAAA CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAAATAACCAAAGTAACTAATCCACT GGGCCTCAGCATAGATTTTCGCTTAGGGCCCCAGAAATGCGAGGACCAGCCATGTCTAGTG GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG TTATTATTCTTTAGATATTATTTAATTTTTTGGAAAAATAACAAACTTATACTTTTTGTGTA TTATTATTTAGATATTTAATTTTAGGAAAAATAACAAACTTATACTTTTTGTGTA CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTTCGGATGGCCCA CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT CTTCTTCTGCCTTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG TTCAAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGAGT ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCCTTTCGGATGGCCCA CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC Conservative ITTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 94.0%; 100.0%; CGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA Score 1311; D; Pred. No. 0; 0; Mismatches ВB 8 0 CTTTCAAAGAATTTTGATTTT Length Indels 0 Gaps 840 660 600 600 540 300 960 960 900 900 840 780 780 720 720 660 540 480 480 420 420 360 360 300 240 180 180 120 60 120 0

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Male tissue-preferred regulatory region
Patent: WO 0160997-A 9 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                               CAACTTCCATGCAAACACGCACATATGTTTCCTGAACAGATCTATTAAAGATCACAACAG
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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RESULT 9
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Best Local Similarity 100.0%;
Matches 111; Conservative
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Location/Qualifiers
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                                                                                                                                                                          h 3.6%; So Similarity 100.0%; F 50; Conservative 0;
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/mol_type="unassigned
/db_xref="taxon:4577"
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                                                                               AC149836.1 GI:49035067
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
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Zea mays clone ZMMBBc0496L17, *** SEQUENCING IN PROGRESS ***
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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clade; Panicoideae; Andropogoneae; Zea.
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llarity 100.0%; Pred. No.
Conservative 0; Mismatc
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                                                 /db_xref="taxon:4577"
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35256: gap of 100 bp
97940: contig of 62684 bp in length
98040: gap of 100 bp
114817: contig of 16777 bp in length
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RS Biren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, V., Bloom, T., Boguslavkiy, L., Arachchi, H.M., Barta, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Arachchi, H.M., Barta, N., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreita, P., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreita, P., Dooley, K., Dorris, L., Erickson, J., Faro, S., Graham, L., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pherre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Grand-Pherre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Mayor, J., Marthews, C., McCarthy, M., Meldrim, J., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talers, M., Yusasiliev, H., Venkataraman, V.S., Viel, R., Voa, Misson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                           1 (bases 1 to 114817)
Birren,B., Nusbaum,C., Lander,E.,
and Messing,J.
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Contact: sequence_submissions@broad.mit.edu
                                               Web site: http://www-seq.wi.mit.edu
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Jersey, 190 Freingurys......(http://pgir.rutgers.edu)
(http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
Tucson, Project Information Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (htm.//mir mirgar edm) NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. Center clone name: 496_L_17 University of New 08854, USA

'Qualifiers

DNA"

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PUBMED
REFERENCE
AUTHORS
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Lykidis, A., Bhattacharayya, A., Bartman, A., Gardner, W., Grechkin, G.,
Zhu, L., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A.,
Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drive, Chicago,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-FEB-2002) Integrated Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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15586"
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number="3.4.11.-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EC_number="2.6.1.62"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=:/
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="FN1001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
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/EC_number="2.8.1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="FN1002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 4585
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                                                                   P1 precursor"
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RESULT 13
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     DEFINITION
                                                AC113237/c
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Matches
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                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                        872 AAAATAGAAAAACACTTAGAAAAAT 895
AC113237 184509 bp Canis familiaris clone RP81-70J12,
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                           AAAATAGAAAACACTTAGAAAAAT 2742
                                                                                                                                                                                                                                                        1.7%; Score 24; DB 1; larity 100.0%; Pred. No. 1.2; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="FN1005"
/codon_start=1
/transl_table=11
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/codon_start=1
/transl_table=1
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IFLIIYISSGQKIRMLQKVYDFASKEEVNNLDETESLTELYTPKPKYIFTRKFFINWD
GSLNIFILEDLEKYEYKKYNYFFIYGTKLLHLKNGKXKKIRYAGPDENEWRKRNFIV
KKNSNIEGKVEYHINLPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8863. .9261)
/gene="FN1006"
/EC_number="2.3.1.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical protein"
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/dbc.xref="GI:19714586"
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YHRYAVFVWNEDTGHFYGFPELLMTPSNSSKKAAIKLAKKEFRRIGNADGLDIKATNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="FN1005"
8337. .8810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mpkkvlfskefildksfelfkeegiesisarnvgkildaspapi
yksissmknikkelikkakdleieyltkkrtgikfldigmgisifareekqlfiqvfs
koniegslidefikkakdleietyltakekqeellvscwvfahglstliatgffk
koniegslidefikvlrdaparlfyeyienysk"
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7577. .8143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIDSKREAWGYGFQLGVNYKVNDKLNLAARYDSRIKMNFKAKGHEHQLETTDILKQTI
GLSTFYFQYTINSKIRRDLPAILSVGASYKVADNYLVSTTANYYFNHQAKMDRVTTFG
EHEHGRDYKNGWEIAVGNEYKLNDKFTLIGSLNYANTGAKTASYNDTEYALNSFTLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MECKIIKNDTNYNLNDLTKLLNTSYWAKDRKKETVKKTVEKSLC
YFAYDTDKNKLIGFARAITDYTTNYYLCDIIVDEEYRGKGIGKKLVETLINDEDLIQV
RGLLITKDAKKFYEKFGFYNKEDVMQKDKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8863. .9261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Acetyltransferase"
/protein_id="AAL95202.1"
/db_xref="GI:19714587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIWDGGLRYIVVMGTNKKTGKWEAFTKFEVDDENIKILINKCSETCDNCDFSWSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transT_table=11
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/db_xref="GI:19714585"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="FN1004"
7577. .8143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .10317
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  WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                        <u>.</u>
                                                                                                                                                                                                                                                                                                           Length 10384;
                        linear
                          HTG 07-AUG-2002
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VERSION
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SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Lee-Lin, S.-Q., Legaspi, R., Maduro, D.L., Mastrian, S.D., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., McCloskey, J.C., McDowell, J., Schueler, M.G., Stantripop, S., Thomas, J.W., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
                         * NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* is the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Aug 7, 2002 this sequence version replaced gi:18958664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-FEB-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 184509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS PHASE2; HTGS DRAFT. Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ordered pieces.
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AC113237.2 GI:22128672
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Akhter, N., Antonellis, A.,
                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrag; version 0.990319
Consensus quality: 184204 bases at least Q30
Consensus quality: 184261 bases at least Q30
Consensus quality: 184224 bases at least Q30
Consensus quality: 184294 bases at least Q20
Insert size: 162000; agarose-fp
Insert size: 164309; sum-of-contigs
Quality coverage: 10.51x in Q20 bases; sum-of-contigs
Quality coverage: 9.24x in Q20 bases; sum-of-contigs
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 184509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: nisc zoo@nhgri.nih.go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.nisc.nih.gov
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AC098210/c
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Best Local Similarity
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RS Muzny, D.Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavzos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Esoctto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., M., Hernandez, J., Jackson, A., Hollins, B., Howells, S., Hullyk, S., Hume, J., Idlebird, D., Jackson, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone CH230-176E2, WORKING DRAFT SEQUENCE.
AC098210
AC098210.8 GI:30581396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the accession number will be preserved.

1 127823: contig of 127823 bp in length
127824 127923: gap of unknown length
127924 147441: contig of 19518 bp in length
147442 147541: gap of unknown length
147542 184509: contig of 36968 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAGGGAGAGAGAGAAGAAA 23269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 212621)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment
clone_end:SP6
vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
129971. .184509
/note="clone overlaps with GenBank Accession Number
AC113567 clone RP81-265M12 (center project name cio)"
147542. .184509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="clone overlaps with GenBank Accession Number AC110671 clone RP81-69D24 (center project name avw)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127924.
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/db_xref="taxon:9615"
/clone="RP81-70J12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .184509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .147441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 2;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212621 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                            Fan,G.,
M., Foster,P.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapathy, K., Kelly, S., Kelly, S., Kelly, S., Kowi, C., King, L., Kowic, C., Kowic, C., Kowic, C., Kowic, C., Kent, C., L., Lebwi, L., Liu, J., L
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TITLE
JOURNAL
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AUTHORS
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

NOTE: Estimated insert size may differ from sequence length

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REFERENCE
AUTHORS
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AC110715/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                               RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyaeji, A., Ayodeji, M., Baca, E., Baden, H., Anyaelebechi, V., Aoyaeji, A., Ayodeji, M., Baca, E., Baden, H., Ballen, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Beryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavzos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Detgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farseer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunarratne, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hamil, C., Hamilton, C., Hamilton, K., Hollins, B., Howells, S., Hulky, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jang, H., Johnson, R., Johnson, R., Jolivet, A., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Longar, J., Liu, J., Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           848 AAAATTAGTTTATTTTCTCTTTAT 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC110715.5 GI:25072769
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-155J23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC110715
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 21821: contig of 212621 bp in length.
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NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 213753)
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clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/clone="CH230-176E2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.7%; Score 24; DB 2; Length 212621;
100.0%; Pred. No. 1.1;
tive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 2550
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SEQUENCING IN PROGRESS
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ORIGIN

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AL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23680201.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entiraly of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., Regier, M.A., Regier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-EEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 213753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C
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-- Genome Center
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TITLE JOURNAL REFERENCE AUTHORS TITLE

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COMMENT

REFERENCE AUTHORS

TITLE JOURNAL

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/enbank draft data.l

* NOTE: This is a "working draft' sequence. It currently

* Consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

data.html).

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Search completed: September 16, 2005, 15:25:40 Job time : 4107 secs
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                                                                                                                                        Query Match 1.7%; Score 24; DB 2; Length 213753; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                              misc_feature
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                                                                   * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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212626 212725: gap of unknown length
212726 213753: contig of 1028 bp in length.
Location/Qualifiers
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clone_end.Sp6"
5028._5742
/note="clone_boundary
clone_end.Sp6
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33891. .35390
/note="wgs_contig"
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1586._.2703
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/mol_type="genomic DNA"
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ALIGNMENTS

RESULT 1 AAX07409 Ms45; male; tissue-preferred; plant tissue; differentiated; AAX07409 standard; DNA; 1394 BP. WPI; 1999-105628/09. Albertsen 23-JUN-1997; 19-JUN-1998; 30-DEC-1998 W09859061-A1 Zea mays. Zea mays Ms45 male tissue-preferred regulatory region 08-JUN-1999 AAX07409; (PION-) PIONEER HI-BRED INT INC MC (first entry) 97US-00880499. Fox TW, 98WO-US012895 Garnaat CW, regulatory region; plant cells; hybrid seed; fertility; ss. Huffman GA, TL;

The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue-preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile

New nucleic acid encoding a - useful in mediating plant

Ms45 male tissue-preferred regulatory region fertility, especially hybrid seed production.

Claim

3; Page 23-24; 39pp; English.

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                                   TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTAGTTTG
                                                                             TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT
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                     TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG
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AAH76333 standard; DNA; 1394 쁌

AAH76333;

29-OCT-2001 (first

Z. mays Ms45 male tissue-preferred regulatory region encoding

Ms45; male hybrid seed tissue; regulatory region; transcription; male fertility;

WO200160997-A2

23-AUG-2001

13-FEB-2001; 2001WO-US004527

15-FEB-2000;

2000US-00504487

(PION-) PIONEER HI-BRED INT INC

Albertsen Š, Fox ΨŢ. Garnaat Š Huffman Ģ Kendall

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2001-514772/56.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

Claim 4; Page 47; 50pp; English.

RESULT 2
AAH76333
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AC A The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The the the The of.

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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably

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    mays Ms45 male tissue-preferred regulatory region encoding DNA.

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15-FEB-2000; 2000US-00504487 13-FEB-2001; (PION-) PIONEER Š, 2001WO-US004527 Fox HI-BRED W. INT INC Garnaat CW, Huffman

A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant. comprising nucleotide the MS45 gene useful f for

2001-514772/56

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4. Page 46; 50pp; English.

The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from Ņ mays an Ms45 male of.

Sequence 1394 BP; 411 ð 311 Ç 231 ဂ္ 441 ; 0 Ç 0 Other,

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TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG

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                                GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
                                                                                                 TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG
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  Query Match
Best Local Similarity
Matches 240; Conserv
                                                                                                                                                 The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                        A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                        Sequence 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514772/56.
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                                                                                                                                                                                                                                                                                                                                                                                             Example
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 mays Ms45

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                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present squence represents a DNA fragment -38 to -195 bases upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                     Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;

    mays Ms45 male tissue-preferred regulatory region fragment.

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  108
                                                                                                             48
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                                                                                                                                           TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGAGATACCTACTCCCAAACAAT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAGCGTTCTCCCGCTAGCTTCCCTCTCCTCCTGCCGATCTTTTTCGTCCACCACCACC
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                                                                                                       TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOX TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 158
                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garnaat CW,
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                                                                                                                                                                                                                                                  Pred. No. 1
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huffman
                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                  .1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ຸດ
                                                                                                                                                                                                                                                                          Length 158
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                                                                                                                                                                                                                  Gaps
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RESULT 7
AAH76336
ID AAH7
XX AAH7
XX AAH7
XX AAH7
XX AAH7
XX AAH7
XX BA AH7
XX M845
XX ABA
XX
                                                                                                                                                                                                                                                                                    RESULT 8
AAH76337
ID AAH7
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Best Local Similarity
Matches 50; Conserv
                                                 Ms45; male tissue;
hybrid seed; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -111 bases upstream of the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A male tissue-preferred regulatory region essential for initiating transcription of
Zea mays

    mays Ms45 male tissue-preferred regulatory region fragment

                                                                                                                                                                                    29-OCT-2001
                                                                                                                                                                                                                                     AAH76337;
                                                                                                                                                                                                                                                                                       AAH76337 standard; DNA; 40 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mediating fertility in a male plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514772/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z. mays Ms45 male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2000; 2000US-00504487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PION-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2001; 2001WO-US004527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 BP; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         веquence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d8.
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                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue-preferred regulatory region
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                                                                         regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RRESULT 9
RAH76315
ID AAH76
XX AAH77
XX AAH77
XX AAH77
XX B9-O
DT 29-O
DX Z- m
XX M945
XX M945
XX M920
PM WO20
PM WO20
PM 15-F
XX D15-F
PM Albe
PM A M8
PM B868
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Best Local :
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A male tissue-preferred regulatory region essential for initiating transcription of
                                                                                                                                                                                                                                                       13-FEB-2001; 2001WO-US004527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          M845; male tissue;

    mays Ms45 male tissue-preferred regulatory region fragment.

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                                                                                                                                                                                                                                                                                                   23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                          Zea maye
                                                                                                                                                                                                                                                                                                                                                                                                                                     hybrid seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH76335 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 32; 50pp; English.
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                                                                      WPI; 2001-514772/56
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                                                                                                                Garnaat
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Pred. No.
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                                                                                                                Huffman
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thes 0;
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  the MS45 gene useful f
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                                                                                                                Kendall
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Best Local S
                                                              pathogen,
caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -152 to -181 bases upstream the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
The invention relates to sclerotina-inducible genes and promoters of initiating transcription from sunflower. The polynucleotides as
                                                                         New genes and promoters from Helianthus annuus, for genetically manipulating plants to enhance disease resistance or resistance pathogen, and for producing proteins for controlling plant disease
                                                                                                                                                                                                                                                                                                                                                                                                                                Sunflower; chitinase; lipid transfer protein; LTP; transcription; sclerotina; genetic engineering; disease resistance; insecticide; antifungal; viricide; nematocide; antimicrobial; antibacterial;
                                       Claim 1;
                                                                                                                                                      Bao
                                                                                                                                                                                                                                         08-AUG-2001; 2001WO-US041629
                                                                                                                                                                                                                                                                                                                                                   CAAT_signal
                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; gene; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sunflower chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30
                                                                                                                             WPI; 2002-269194/31.
                                                                                                                                                                                                     07-AUG-2001;
                                                                                                                                                                                                                11-AUG-2000;
                                                                                                                                                                                                                                                                  21-FEB-2002.
                                                                                                                                                                                                                                                                                                                              TATA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                          WO200214502-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence
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                                       4;
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2001US-00923844.
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Pred. No.
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                                                                          resistance to plant diseases
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RESULT
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Best Local S
Matches 23
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for genetically manipulating plants to enhance disease resistance or resistance to insect, fungal pathogens, viruses or nematodes. The nucleotide sequences are also useful as genetic markers in disease-resistance breeding programs. The polymucleotides are also useful for producing proteins useful in compositions. The compositions are useful reducing or eliminating damage to plants caused by plant pathogens. The compositions find use in agricultural and pharmaceutical compositions as antifungal and antimicrobial agent. For agricultural purposes, the compositions may be used in sprays for control of plant disease. As pharmaceutical compositions, the agents are useful as antibacterial and antimicrobial treatments. The present sequence represents the promoter fragment of the sunflower chitinase gene
                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate pharmacogenomic
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                                                                                                                                                                                                            Page 10900; 11750pp;
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; 2000US-0207454P.
; 2000US-0211314P.
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                                                                                                                                                                                                                                                    nucleic acid molecule associated with cancerous state and correlating with presence of prostate cancer, usef presence of prostate cancer.
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Pred. No.
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Matches 21
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring an displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a pati; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483447/52.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                       expression
                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic expression in human fetal liver.
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                                                                   Similarity
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llarity 100.0%;
Conservative
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-034687P.
2000US-0234359P.
2000US-030359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                              ВP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
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                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                              86 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                           7172; 639pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression;
                                                                                                                              Ç
                                             <u>,</u>
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                                                                 Score 21;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 G; 143
                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid probe #7172.
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                   ŏ.
                                                                                                                            154 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              뮸
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 U;
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                                                                                                                                                                                                                                                                                                                                                                                                                           acid probes useful for analyzing
                                                                                                                              0
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                                                                                     Length 459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 Other;
                                                                                                                              0
                                                                                                                                                                                                                                                     predicting, measuring and rom human fetal liver. The
                                                                                                                              Other;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                           0,
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                                                                                                                                                                                              :he printed from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe;
                                           Gaps
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RESULT 14
AAK32768/c
ID AAK327
XX
AC AAK327
XX
DT 06-NOV
XX
Human
XX
KW Human;
KW microa
XX
OS Homo 8
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                                                                                                                                                                                                                                                                     RESULT 13
AAI38581/c
                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP) The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                            gene
          Homo sapiens
                               microarray;
                                          Human;
                                                             Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                   06-NOV-2001
                                                                                                                            AAK32768
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI38581 standard; DNA; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #7267 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                      1037
                                                                                                                                                                                                                                                                                                                                                                         n genome-derived single exon nucleic acid probes useful for analyzing expression in human placenta.
                                                                                                                                                                                  118
                                                                                                                                                                                                                                                                                                                                                      25; SEQ ID NO 7267; 654pp; English.
                                          bone
                                                                                                                                                                                                                         ch 1.5%; Sc
l Similarity 100.0%; P
21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder;
                                                                                                                            standard;
                                                                                                                                                                                                     AAAGGGAGAGAGAGGAAGA 1057
                                                                                                                                                                                 AAAGGGAGAGAGAGAAGA 98
                                                                                                                                                                                                                                                                    459 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel
                               marrow expressed excancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312P
2000US-0207456P
2000US-00638408
2000US-00632365
2000US-0234687P
2000US-0236359P
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                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                  86 A; 149 C; 70 G; 154 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to measure
                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Chen
                                                                                                                             459
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                                                                                                                            ВP
                                                                                                                                                                                                                                   Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression in human placenta sample.
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                                        exon;
                              con; gene expression analysis; probe;
lymphoma; myeloma; ss.
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20;
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                                                                                                                                                                                                                                             Length 459;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0236359P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                          30-JAN-2001;
                                                                                                               09-AUG-2001.
                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarray;
                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                        05-NOV-2001
                                                                                                                                                                                                                                                            AAK07027;
                                                                                                                                                                                                                                                                                 AAK07027 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression in human bone marrow.
                                                                                                                                  WO200157275-A2
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                    Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4;
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                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention provides a number of single exon nucleic ac
                                                                                                                                                                                                                                                                                                                                             1037 AAAGGGAGAGAGAGGAAGA 1057
                                                                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SG,
                                                                                                                                                                                                                  brain expressed single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome-derived single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7325; 658pp +
        2000US-0180312P.
2000US-0207456P.
2000US-0060840B.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-0236359P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 86
                                                                                          2001WO-US000667
                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                       100.0%; --
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                                                                                                                                                                                                                                                                                  459
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Pred. No
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                                                                                                                                                                                                                   SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                   U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes
                                                                                                                                                                                                                                                                                                                                                                           <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                             Length 459;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                    7018
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                                                                                                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             of cancers
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: September 16, 2005, 13:08:40 Job time: 579.5 secs
                                                                                                                                                                                                                                        Query Match 1.5%; Score 21; DB 4; Length 459; Best Local Similarity 100.0%; Pred. No. 20; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                Sequence 459 BP; 86 A; 149 C; 70 G; 154 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 7018; 650pp + Sequence Listing; English.
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                                                                                                                    Hanzel DK,
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Result
No.
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
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eeq length: 2000000000
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Gapop 60.0 , Gapext 60
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12923.341 Million cell updates/sec
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1394
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Query Mat Best Loca Matches 1	Sequence 2, Application US/08880499 Patent No. 6037523 GENERAL INFORMATION: APPLICANT: Albertson, Marc C. APPLICANT: Fox, Tim W. APPLICANT: Fox, Tim W. APPLICANT: Huffman, Gary A. APPLICANT: Huffman, Gary A. APPLICANT: Kendall, Timmy L. TITLE OF INVENTION: MALE TISSUE TITLE OF INVENTION: AND METHOD NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Dorwin Building, 7100 STREET: Box 1000 CITY: Johnston STRATE: IOWA COUNTRY: USA ZIP: 50131 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-I SOFTWARE: Patentin Release #1 CURRENT APPLICATION NUMBER: US/08/88-I SOFTWARE: Patentin Release #1 CURRENT APPLICATION: 800 ATTORNEY/ACENT INFORMATION: NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 0578 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4844 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1394 base pairs TYPE: nucleic acid STRANDEDNESS: Bingle TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)		44	42 43	40 41	39 8	35 37		322 0
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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                                                                                                                                                                                                 APPLICATION NUMBER: US/08/880,4
FILING DATE: CONCURRENTLY HEREW
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
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PATENT NO. 6037523
GENERAL INFORMATION:
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
Query Match 94.0%; Score 1311; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1311; Conservative 0; Mismatches
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STREET: Darwin Building, 7100 N.W.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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LENGTH: 1394 base pairs
TYPE: nucleic acid
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APPLICANT: Carl, Garnaat W.
APPLICANT: Kendall, Timmy L.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
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GENERAL INFOMATION:
GENERAL INFOMATION:
APPLICANT: VENTER, J. Craig et al.
FITTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
FILLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,488
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VENTOR FILING DATE: 2000-09-0
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G
TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR TILING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 124481
LENGTH: 601
TYPE: DNA
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; Sequence 124481, Application US/09949016
; Patent No. 6812339
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; ORGANISM: Human
US-09-949-016-13563
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNOWN GENES
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OF DETECTION
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; ORGANISM: Human
US-09-949-016-147075
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5912413
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application Patent No. 5912413
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 147075
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 601
             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DM COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,784A
APPLICATION NUMBER: US/08/410,784A
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEB: Weingarten, Schurgin, Gagnebin and Hayes LLP
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: JAMES,
                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   817 TTTCTTTCAAAGAATTTTGA 836
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Pred. No.
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US-09-949-016-15250
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15250
LENGTH: 21679
                                                                         Matches
                                                                                      Query Match
Best Local (
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Best Local Similarity 100.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: 62070-89-09
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                  TYPE: DNA
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REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: ISU-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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4880 GATTTTTCTTTTCATTCTT 4899
                     630 GATTTTTCTTTTTCATTCTT 649
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ilarity 100.0%;
Conservative (
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US-09-949-016-12426/c

Sequence 12426, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

RESULT 8

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
IITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
IITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-17933/c
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US-09-949-016-15868
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
Sequence 17933, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Patent No. 6812339
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SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 12426
LENGTH: 65424
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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LOCATION: (1)...(65424)
OTHER INFORMATION: n =
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100.0%; Pred. No. 13;
ive 0; Mismatches
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Pred. No.
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OF DETECTION AND USES THEREOF
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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US-09-949-016-41823/c
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Sequence 41823, Application US/09949016

Sequence 41823, Application US/09949016

Patent No. 6812339

Patent No. 6812339

Patent INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT PILING DATE: 2000-04-14

CURRENT PILING DATE: 2000-04-14
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CURRENT APPLICATION UNMEBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PRILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PRILING DATE: 2000-09-08
PRIOR PRILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17933
LENGTH: 601
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Best Local Similarity
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ORGANISM: Human
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19; Conserv
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100.0%; Pred. No.
Live 0; Mismatcl
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100.0%; Pred. No.
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PRIOR FILING DATE: 2000-10-20

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US-09-949-016-145344/c
US-09-949-016-145344/c
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/337,768
PRIOR APPLICATION NUMBER: 60/337,768
PRIOR APPLICATION NUMBER: 60/331,498
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 41823
LENGTH: 601
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; ORGANISM: Human
US-09-949-016-41824
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; ORGANISM: Human
US-09-949-016-41823
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Best Local Similarity
Matches 19; Conserv
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Best Local Similarity
Matches 19; Conserv
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
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100.0%; Pred. No. 39;
ative 0; Mismatches
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0; Mismatches
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Search completed: September 16, 2005, 08:14:17 Job time : 178.5 secs
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US-09-949-016-145345/c
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145345
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 145344
LENGTH: 601
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                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                    LENGTH: 601
                                                                                                                                Local Similarity hes 19; Conserv
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100.0%; Pred. No.
                                                                                                                                              100.0%;
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100.0%; Pred. No.
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39;
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

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US-10-73-600-17775
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US-10-73-600-17775 US-10-713-381-4 Sequence 11465, A
Sequence 51470, A
Sequence 7365, Ap
Sequence 21199, A
Sequence 2125, Ap
Sequence 47, Appl
Sequence 47, Appl
Sequence 240, App
Sequence 114007,
Sequence 119819, A
Sequence 119819, A
Sequence 119819, A Sequence 4725, Ap Sequence 4726, Ap Sequence 4726, Ap Sequence 3728, A Sequence 37438, A Sequence 134230, Sequence 134230, Sequence 1729, Ap Sequence 1775, A Sequence 1775, A Sequence 1775, A Sequence 1744, App Sequence 274, App Sequence 675, App Sequence 5, Appli Sequence 355, App Sequence 56524, A Sequence 1, Appli Sequence Sequence Sequence Sequence 183040, Sequence 117183, Sequence Sequence Sequence Sequence 4, Appli 139460, 139461

ALIGNMENTS

RESULT 1 US-10-713-381-2

Sequence 2, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:

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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARL W.
APPLICANT: HUFFWAN, GARY
APPLICANTON: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea may8
US-10-713-381-2
Query Match
Best Local Similarity 100.0%; Score 1394; DB 20; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1394; Conservative 0; Mismatches 0; Gaps 0
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US-10-713-381-6	US-10-713-381-5	US-10-739-930-1857	US-10-713-381-3	US-10-713-381-9	US-10-713-381-1	US-10-713-381-2	Length DB ID
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: APPLICANT: ALBERTSEN, MARC C.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
FITTLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
FITTLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION STATE 1997-66-23
NUMBER OF SEQ ID NOS: 24
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LEMENT: 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.0%; Score 1311; [Best Local Similarity 100.0%; Pred. No. 0; Matches 1311; Conservative 0; Mismatches
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                                              TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260
                                                                                               GGTTCGGCAGCTCTCGTGTCATCTCACATGCCATACCTACATGCTTCGTTCAACCGTTCGTC
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RESULT 3 US-10-713-381-9 ; Sequence 9, Application US/10713381 ; Publication No. US20040221331A1 ; GENERAL INFORMATION:

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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
ITILE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
ITILE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
ITILE OF INVENTION: USING SAME
ILLE REFERENCE: 578R
CURRENT FALLING DATE: 2003-11-14
CURRENT FILLING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 255
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-9
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER: OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 158
TYPE: DNA
ROANISM: Zea mays
US-10-713-381-3
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Sequence 3, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GRANAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD FILE REFERENCE: 578R
FILE REFERENCE: 578R
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                                                                                Query Match 8.0%; Score 111; DB 20; Best Local Similarity 100.0%; Pred. No. 6.2e-45; Matches 111; Conservative 0; Mismatches 0;
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                  TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCCAAACAAT 1260
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CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-5
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; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-CLUSTER1429_US-10-739-930-1857
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US-10-739-930-1857
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Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: KOVALIC, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)B
FULE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 1857
LENGTH: 1663
                                                                                Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNART, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1229 CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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                                                                                Conservative
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100.0%; Pred. No. 1.2e-21;
vative 0; Mismatches 0;
                                                                                                  3.6%; Score 50; DB 20; 100.0%; Pred. No. 3.3e-14;
                                                                                0
                                                                                Mismatches
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US-10-713-381-4
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                                                                                                                                                                                   US-10-713-381-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                    Query Match 2.2%; So
Best Local Similarity 100.0%; F
Matches 30; Conservative 0;
                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                 LENGTH: 30
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 40
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                       1179 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.9%; Score 40; DB 20;
100.0%; Pred. No. 3.5e-09;
                                                                                                            Score 30; DB 20; Pred. No. 0.00038;
                                                                                       Mismatches
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RESULT 9 US-09-923-844B-5/c

Sequence 5, Application US/09923844B Patent No. US20020166143A1 GENERAL INFORMATION:

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APPLICANT: Bao, Zhongmeng
APPLICANT: Lu, Guihua
TITLE OF INVENTION: Sclerotinia-inducible Genes and
TITLE OF INVENTION: Promoters and Their Uses
FILE REFERENCE: 35718/234631
CURRENT APPLICATION NUMBER: US/09/923,844B
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/224,603
PRIOR APPLICATION NUMBER: US 60/224,603
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
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US-10-357-930-56524
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Sequence 56524, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

APPLICANT: Hondshan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,

TITLE OF INVENTION: UDANTIFICATION, ASSESSMENT, PREV

FILE REFERENCE: MRI-007BCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 355, Application US/10085117 Publication No. US20030232334A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 194945
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REPERENCE: 529452000121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morris, David W. APPLICANT: Engelhard, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pioneer Hi-Bred International, Inc APPLICANT: Bao, Zhongmeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 849
TYPE: DNA
ORGANISM: Helianthus annuus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: variation
LOCATION: (1)...(194945)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                        28972 TGCATGATCTCCATGTTCCACT 28951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  556 AGTITATTTTCTCTTTATAAAT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854 AGTTTATTTTCTCTTTTATAAAAT 876
                                                                                                                                                                                                                                                                                                                                                113 TGCATGATCTCCATGTTCCACT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%; Score 23; DB 9; ilarity 100.0%; Pred. No. 1.7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%;
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                                          PREVENTION, AND THE
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RESULT 13 US-10-425-115-117183/c

Sequence 117183, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas APPLICANT: Kovalic, David APPLICANT: Zhou, Yihua

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; ORGANISM: Homo sapiens
US-10-357-930-56524
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CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR FILING DATE: 2003-02-16
PRIOR FILING DATE: 2000-02-17
PRIOR PPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR PRIOR PRICING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                            APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 183040
LENGTH: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 183040, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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LENGTH: 333
                                                                                Matches
                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/219,007 PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                    OTHER INFORMATION: Clone ID: MRT4577_98517C.1
                                                                                                                                                                                                          ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                    Local Similarity
                                       632 TITTTCTTTTCATTCTTGTT 652
                                                                              21;
  72
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                                                                                Conservative
                                                                                                    100.0%;
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100.0%; Pred. No.
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100.0%; Pred. No.
                                                                                0; Mismatches
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                                                                                                                          DB 20;
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                                                                                                                       Length 356;
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                                                                                0;
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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules a
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 117183
; LENGTH: 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Clone ID: MRT4577_3835C.1 US-10-425-115-117183
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Best Local S
Matches 21
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                     PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
PRIOR
PRIOR
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PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408
                                     APPLICATION NUMBER: US 60/234,687
                                                                            APPLICATION NUMBER: PCT/US01/00670
                                                                                             FILING DATE:
                                                                                                               APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                    FILING DATE:
                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                    FILING DATE: 2001-01-30
                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00667
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Search completed: Job time : 1293.5

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US-10-425-115-51470/c
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                                                                                                                                                                                                            SEQ ID NO 51470
LENGTH: 1203
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(1203)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51470, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Best Local Similarity
Matches 21; Conserv
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11465
                                                                          Matches
                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO ACOOO100.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.2
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

60	1 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAAA	Db
463	404 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAAA	82
0;	y Match 65.1%; Score 908; DB 9; Length 963; Local Similarity 100.0%; Pred. No. 0; hes 908; Conservative 0; Mismatches 0; Indels 0; Gaps	Query Match Best Local : Matches 90:
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	/db_xrer="taxon:45//" /clone="zMvBMa0554D15"	
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	Class: sheared ends.	
	Seq primer: TR	
	Fax: 301-838-0208	
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	9712 Medical Center Drive, Rockville, MD 20850, USA	
	Contact: Cathy Whitelaw TIGR	
	Other_GSS8: OGWDQ20TV	COMMENT
	Unpublished (2002)	JOURNAL
	Consortium for Maize Genomics	TITLE
•	Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.	
	Respick A Frager C M Budiman M A Redell T A Doblifing T	AULIONO
		REFERENCE
į	clade; Panicoideae; Andropogoneae; Zea.	
γca;	sukaryota; Viridipiantae; Streptopnyta; Embryopnyta; Tracneopnyta;	
•		ORGANISM
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	CC656933.1 GI:32060225	VERSION
	genomic survey sequence. CC656933	ACCESSION
	OGWDQ20TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15,	DEFINITION
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Tel: 301-838-0208
Email: whitelaw@tigr.org
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; PAclade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 915)

Whitelaw.C.A., Ouackenbush.J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)
Other GSSs: OG1AG08TH Contact: Cathy Whitelaw
                                                 TGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAA
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/mol type="genomic DNA"
/strain="By3"
/db_xref="taxon:4577"
/clone="zwMBMa0716B15"
/clone="ib="Zm/O.71.5 KB"
/note="Vector: DBCSK-; Site 1: HincII; 0.7-:
methylation filtered genomic DNA library"
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JOURNAL
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CC656939
CCGDQ20TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence.
CC656939
CC656939.1 GI:32060231
GSS.
Zea mays
Zea m
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGWDQ20TM
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Class: sheared ends.
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9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
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                            TTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTT 1202
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/clone 11b="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.
methylation filtered genomic DNA library"
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/strain="B73"
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Pred. No. 1.1e-197;
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Zea mays
Zea mays
Eukaryota;
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                                                                     BE828689 539 bp PUFHM74TB ZM_0.6_1.0_KB Zea mays genomic survey sequence.
BE828689
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1 (bases 1 to 878)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGLACOBTV
                                                          BZ828689.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cathy Whitelaw
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/clone=1ib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1:
methylation filtered genomic DN
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/strain="B73"
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 Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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100.0%; Pr
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J. 5.5e-22;
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                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 611)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                           BZ828694
PUFHM74TD ZM_0.6_1.0_KB
genomic survey sequence.
BZ828694
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1 (bases 1 to 539)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
                                                                                                                                                                                                                    Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUFHM74TB
                                                                                                                                                                                                                                                                                                                                                                                               GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize Genomics Consortium Unpublished (2003) Other GSSs: PUFHM74TD
                                                                                                                             Email: whitelaw@tigr.org
                                                                                                                                                            9712 Medical Center Drive, Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Tel: 301-838-5843
                                                                                                  Class: sheared ends.
                                                                                                                Seq primer: TF
                                                                                                                                                                                                      Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
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                           /mol_type="genomic DNA"
/strain="B73"
                                                                                   Location/Qualifiers
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/clone="lib="ZM_0.6_1.0 KB"
/clone="Vector: pCR4-TOPO; Site_1:
/note="Vector genomic DNA library"
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 /clone="2MMBTa320N03"
                                                         organism="Zea mays"
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               xref="taxon:4577"
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Best Local Similarity
Matches 27; Conserv
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GSS.
Zea mays
Zea mays
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Zea mays
                                                genomic survey sequence
CG011564
CG011564.1 GI:33883730
                                                                                              CG011564
ZUABT23TV ZM_3.0_4.0_KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 804)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
CG148339
CG148339.1 GI:34039122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Other_GSSs: PUKBG46TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: TR
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/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                           /clone="ZMMBTa0780G19"
/clone_lib="ZM 0.6_1.0 (KB"
/note="Vector: pCR4_TOPO; Site_1:
/cot selected genomic DNA library"
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/strain="B73"
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100.0%; Pr/
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Pred. No. 0.052;
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Pred. No.
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0.052;
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AUTHORS
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                       Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 854)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics

Unpublished (2002)

Other_GSSs: ZUABT23TH
                                                                                                                          Email: mccombie@cshl.org
Plate: 1e38 row: h column:
Seq primer: -21M13UnivFwd
                                                                                                                                                                                                                                                                                                                                  Rabinowicz, P.D., O'Shaughnesey, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE371637 687 bp DNA 11 1e38h03.b1 WGS-ZmaysF (DH5a methyl filtered) 1e38h03.5', genomic survey sequence.
BE371637
                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 687)
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GSS.
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Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
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                                                                                                        lass: shotgun
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                                                                                     quality sequence stop: 687
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/clone="Ib="ZM_3.0_4.0_KB"
/note="Vector: pBcSk-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
/organism="Zea mays"
/mol_type="genomic DNA"
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/mol_type="genomic DNA"
                                                               Location/Qualifiers
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CC810403/c
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Best Local (
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                     265 CCAGGGGATATATGTCCCCCACAAT 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 726)

1 (bases 1 to 726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C. Rouzard, K., Fuks, G., Yu, Y., Wing, R. and Messing, J. Sequencing of the maize genome at PGIR (2003b) Unpublished (2003)
Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS.
                                                                                                                                                                                                                                                                                                                                                                            Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 732 445 3801 Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University
190 Frelinghuysen Road, Piscataway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dr.Joachim Messing's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence. CC810403
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ZMMBBc0479C04r ZMMBBc Zea mays (
                                                                                                                                                                                                                                                                                                                                                                                                             Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Plant Genome Initiative
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CCAGGGATATATGTCCCCCACAAT 340
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Location/Qualifiers
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/clone lib="MGS-ZmaysF (DH5a methyl filtered)"
/clone lib="MGS-ZmaysF (DH5a methyl filtered)"
/note="Torgan: immature ears; Site_1: Xba I; Site_2: Xba I;
/note="Torgan: immature ears; Site_1: Xba I and one nucleoTide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (:x/y reads in MJ3mp19. b/g reads in pUC19). The same ligation was transformed into DH5a."
                                                                                                                                                                  /clone_lib="ZM
/note="Vector:
                                                                                                                                                                                                     /db_xref="taxon:4577"
/clone="ZMMBBc0479C04"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                               organism="Zea mays"
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/clone="ie38h03"
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100.0%; Pred. No. 0.0
Live 0; Mismatches
                                                                                          100.0%;
                                                                                                                                                                                    _lib="ZMMBBc"
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                                                                      Score 25; DB; Pred. No. 0.5
                                                                                                                                                                pTARBAC1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                          397.
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genomic
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0.55;
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                                                                                                                                                              Site_1: BamHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NJ 08854, USA
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AUTHORS
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CG190606/c
LOCUS
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CG305519/c
LOCUS
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AUTHORS
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Best Local S
Matches 25
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                                                                                                                                                                                                              genomic survey of CG190606 CG190606.1 GI:: GSS.
                                                                                                                                                                                   Zea mays
Zea mays
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Location/Qualifiers
                                         Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUIHP82TD
                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 825)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                   CG190606
PUIHP82TB ZM_0.6_1.0_KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clade; Panicoideae; Andropogoneae; Zea.

(Dases 1 to 819)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
CG305519
CG305519.1 GI:34219733
GSS.
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Other_GSSs: OG0GM20TH
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OG0GM20TV ZM_0.7_1.5_KB
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                   Bennetzen, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Medical Center Drive,
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                            Cathy
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/clone="zMMBMA0713C15"
/clone_lib="ZM_0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%;
                          Whitelaw
                                                                                                                                                                                                                                                         sequence.
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Pred. No.
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Rockville,
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MD 20850, USA
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ZMMBMa0713C15,
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                                                     Query Match
Best Local S
Matches 25
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Best Local (
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582
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
Other GSSs: PUIHP82TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 833)
1 (bases 1 to 833)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Wan Ake
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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Tel: 301-838-5843
Fax: 301-838-0208
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: TF
Class: sheared ends
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Class: sheared
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llarity 100.0%;
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CoT selected genomic DNA library"
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/strain="B73"
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0; Mismatches
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Zea mays
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CC358144 CC358144 GI:30827544 GSS.
                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 878)

1 (bases 1 to 878)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                                                                                                                                                     genomic survey sequence.
CG307825
CG307825.1 GI:34224985
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1 (Dases 1 to 857)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHPY12TB
Unpublished (2002)
Other_GSSs: OGWBG01TV
Contact: Cathy Whitelaw
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167 AAAAAATTAGTTTATTTTCTCTT 143
                          844 AAAAAAATTAGTTTATTTTCTCTT 868
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Class: sheared ends.
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Tel: 301-338-5843
Fax: 301-438-0208
Email: whitelaw@tigr.org
                                                                                 Similarity
                                                              1.8%; Score 25; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                          /organism="Zea mays"
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/strain="B73"
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/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Search completed: September 16, Job time : 4293.5 secs

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ALIGNMENTS

VERSION KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION RESULT 1 AX224395 LOCUS g δ S 밁 片 ORIGIN FEATURES source REFERENCE AUTHORS TITLE JOURNAL Query Match 100.0%; Score 1394; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 4.1e-269; Matches 1394; Conservative 0; Mismatches 0; Indels 0; 181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 121 61 61 AX224395 Sequence 2 AX224395 Zea mays Zea mays 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 2 23-AUG-2001, PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. AX224395.1 CTTCTTCTGCCTTATTACTGACTGAATCGGGGGTTACAAAAAAACTTCCACGGGTGCATGAT CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCCGGTGGTTCCCAT 180 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" 1394 bp from Patent WO0160997. GI:15554637 DNA Indels 0; and Kendall,T.L. of using same PAT 10-SEP-2001 240 120 180 120 60

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1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L.
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                                     AAAGATCACAACAGCTAGCGTTCTCCCGCTAGCTTCTCCCTCTCTCCTCTGCCGATCTTTTT
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           TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT
                                    CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACCACGATCCTCTTAAAAAACCGAAGCTATCATGTATAAAAAAACCAACGATCCTCTTAAAAAACCACGATCCTCTTAAAAAAACCAACGATCCTCTTAAAAAAA
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nilarity 99.8%;
Conservative
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nt: WO 0160997-A 1 23-AUG-2001;
EER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
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/mol_type="unassigned
/db_xref="taxon:4577"
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                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1394)
Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
Kendall, T.L.
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Male tissue-preferred regulatory
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BD062176.1 GI:22607781
JP 2001520523-A/1.
Male tissue-preferred regulatory region Patent: JP 2001520523-A 1 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC PN JP 2001520523-A/1 PD 30-OCT-2001 PF 19-JUN-1998 JP 199504910
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PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
PI TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC
, C07K14/34, C12Q1/68,
PC A0145/00
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
FH Key Location/Qualifiers.
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                    CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA
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/mol_type="genomic DNA"
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Hi-Bred Intl. Inc., 7300 N.W.
IA 50131-1004, USA
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Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
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Fox.T.W., Trimmell,M.R. and Albertsen,M.C.
                                                                                                                                                            Fox, T.W., Trimnell, M.R. Direct Submission
                                                                                                                                                                                                         Cloning of M845, a gene Unpublished
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/organism="Zea mays"
/mol type="genomic DNA"
/cultivar="B73"
/db_xxef="taxon:4577"
/chromosome="9L"
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GRECHWAGSVGTWAGSVAREADGDPIRFANDLDVHRNGSVFFTDTSMRY
SRKOHLNILLEGEGTGRLEKYDPETSGVHVULKGLVFFNGVGISEDHOFTLFSETTNC
RIMRYWLEGPRAGEVEVFANLPGFFDNVRSNGRGQFWVAIDCCRTPAQEVFAKRPWLR
TLYFKFPLSLKVLTWKAARRMITVLALLDGEGRVVEVLEDRGHEVMKLVSSVREVGRK
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                                                                                                                                  Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                          Albertsen, M.C., Fox, T.W., Garnaat, C.W., Male tissue-preferred regulatory region Patent: WO 0160997-A 9 3-AUG-2001, PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Sequence 3 :
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Zea mays clone ZMMBBc0334A01,
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Pred. No. 4.9e-19;
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi H.M., Barna, N., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, S., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maddonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maddonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tawers, M., Vasailiev, H., Venkataraman, V.S., Veil, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Stubet, M., Stojanovic, M., Stubet, M., X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                             Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 17, 2004 this sequence version replaced gi:49658659. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
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Contact: sequence_submissions@broad.mit.edu
                            Web site: http://www-seq.wi.mit.edu
                                                                  Center code: WIBR
                                                                                        ------ Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
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Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
                                                 DEFINITION
                                                                                   POCUS
```

This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html. Sciences West, 448A, P.O. BOX 210000, Uniterior Tucson, AZ 85721, USA (http://www.genome.arizona.edu) (http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box, 21008B, University of Arizona, Center clone name: 334_A Center project name: L30003 Consensus Information

* NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 100617 contig of 100617 bp in length
100718 100717: gap of unknown length
1004731 104830: gap of unknown length
1104331 115104: contig of 10274 bp in length
115105 115204: gap of unknown length
115205 156396: contig of 41192 bp in length
156397 156496: gap of unknown length
156497 179936: contig of 23440 bp in length
119937 1861991: contig of 61618 bp in length
1180037 1861991: contig of 61618 bp in length contig of 6163 bp in length

/db_xref="taxon:4577" /clone="ZMMBBC0334A01" /mol_type="genomic DNA" organism="Zea mays" .186199 'Qualifiers

FEATURES

source

/clone="ZMMBECU334AU1" /clone_lib="CHORI-201 Maize B73 BAC MboI Library"

Matches 115;

Conservative

0

Mismatches

Query Match Best Local Similarity

5.5%;

Score 77; Pred. No.

2.5e-05; 45;

Length 186199; Indels

1.

Gaps

Ś 밁 Ś 밁 162117 TTCTAAGTGAAATTAGTTCATTTTCCTTTAACAAAATAGAAATTTATTGGTAAAATAGAG 162176 162058 CTTTTCTTTTACTTTTAGGGCTAGTTTGGGAACCCTATTT-TTCTAAGAAATTTTTCATTT 162116 840 TTTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAG 900 TTGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAA 940 TTTCCAAACTAACCCTCAAGTATATAATGAATGCAGGACAA 162217 839

RESULT 9 AC117267

AC117267 25769 bp DNA linear INV 21-FEB-2004 Dictyostelium discoideum chromosome 2 map 5836255-5862024 strain AX4, complete sequence. 25769 bp

CDS

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REFERENCE
AUTHORS
TITLE
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CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (09-APR-2002) Genome Analysis, Institute of Molecular Submitted (09-APR-2002) Genome Analysis, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 25769)
Gloeckner, G., Elchinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biotechnology, Beutenberstr. 11, 3 (bases 1 to 25769)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agency :
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//www.uni-koeln.de/dictyostelium/project.shtml
                                                                         /translation="MEFPTKYVYITSNLDKPKEWFTQSEMSLITTTDT1QKSFVNNSG
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GLPPIGGSLNKKSSSSSSSSSSKGKTGLFNKIFSGKUKQPSPQQAASPSTIDRTGQI
STNRLEANVLSYSMSNLSKEVPLITGDCYYCQGCNVILSRFSNLVKTGDDSFTWKCEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deutsche Forschungsgemeinschaft (DFG). Location/Qualifiers
                         CKYSNSNILLEQGEIPNKDSVEYVLSSPSTSSTTDGSKREESIIIYCIDVSGSMGITT
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FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENNKDKLFSSLPFFYLKNIAENQEFEDYY
                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSGSGSSGTSGAQLSGTGYVINHQ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSPLGSWTDFKIKQFKKLNDIETILSDVEVNLCSSSNNNNNNNNVDDETLTLLGSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(832. .1070,1237. .1349,1533. .1798,
1896. .2053,2231. .2360))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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/db_xref="GI:42733681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="GeneID exon scores (in order of location ranges):
23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="5836255-5862024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .25769
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                                                                                                                                                                                                                                                                                                                                                                                    of location ranges):
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TQILFHLRLYNIHANKKVFLFPIQL/DYKFKGYLQSWYLNYHDDNDDDADEDS YDSDI
DDDS YSDGGNCSSSGSSD1GSSSNS INNGI SNSSSSILSNSLLELSMIR RVNSL
PEGLKSIEFEKEYNVIQDRLLFPSISSIFFYGFONDE IAKGVI SDNVLSITFGDSFON
SLDGNWLFKQLKHLQFGKKFQQTI KMGQLPSSLTSLILDPRS YKGVI EIGSI PDS VKT
LDYKKNSCSNQESI S GNPI PKSITRLV GESEFWQNI KANDI SSYNLTSI HFGBERENS
DIGIKSLEPNSI TEIKFGRAFDRD IKLCPSSI TSI DFGNKTNE LSMYTQTLTSI LDFGS
KFNQI I PQGI FIHTKLKSLNFGYHFNQI I PADTLPFTLESLNLGGYNREITVKNDEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MEEKIKFYFEIIDFQNQKFKIQEFTSKLIGLKEESFTTFKPIVY EKYLAWTQSIEESILKTNGTINKSIFEEIFSYCGYIGEFLBYBFIYFKFIILDDYIFEKINSLAMKLAKEKLINSIIYYNNKUBENKIGFEBEIIBFQNFTHKESFQRIINBNYIFKINSLOSPOSSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSINGSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSIDSKUSITUSIDSKUSIDSKUSIDSKUSIDSKUSI
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PNNAPIKKNSVGII (GNGPNVNNNKDRKLNSNDGVNFGKKNILETPSKNSNVSTYKHS
SSSSSLLAKNBYDIBSIKKELKSMDISTGGISPLSSPLRESSPISTIDLESITATTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="similar to Dictyostelium discoideum (Slime mold). Hypothetical 97.7 kDa protein"
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KNSNHWMMPSLKINQIINDNNNNISNINFVQIQSNSSSLSSSCSTYQSCPIEDEHIQE
QLRIQKEQLKQIDDDDDDDDDDDDDDSSPSPPPPTTTKTFCLSPRPIIKKEENID
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Hypothetical protein"
/protein_id="AA338627.1"
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/db_xref="GI:42733686"
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23.29 - GSCJ_ID dd_00728"
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ENYDWTGIPFNEKEVEASNNESTEESTLEKEMNKLEISEENENHNN"
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/protein_id="AAS38628.1"
/db_xref="GI:42733684"
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/note="GeneID exon scores (in order
10.37, 128.60 - GSCJ_ID dd_00729"
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TDVEMSICLHPTLEINKYDSKQGLSRVVKQFPWNSLIDLTLLYSSNAPTEFVQIYF
FQIQIKYTKLDGVRCLRVVSAQLQATPDFNTSTSNANI SILAMAFTQQAAKIAQQQEY
MESRLHLKAATKLIRSLCNTDEQWEEFYNFEVLREEMEAPLITCIKNKQQRVEKAATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(12884. .13020,13172. .15320)
/note="GeneID exon scores (in order of location ranges):
/2,42, 136.56 - GSCU_ID dd_00727"
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/protein_id="AAS38629.1"
/db_xref="GI:42733685"
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68.61 - GSCU_ID dd_00752"
/codon_start=1
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TTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATT
                                             ATAAAATATTAATTAATTAAA-ATTATTTTCTTATTTTTATTTTAATTGAAAAAT
                                                                                                                                         AGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATAGGAAAGGTAAG
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                                                                                         CTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTGTTATTGTTTTTATATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="hypothetical protein"
/protein_id="Ass38632.1"
/protein_id="Ass38632.1"
/protein_id="Ass38632.1"
/db_xref="ci;42733688"
/translation="MDNNNLPQPYPPQSNNYCDCDDNENGNDSTLTIQPKPIAPSLPS SQD985TI15Q1NNKYQLFKEFKEHNNIDSNMLCVQLSEFQISFKTATNTFDSWLN SLWLPPTGFKKL/DNHLKKVYIFPKSFKHNNIDSNGMLCVQLSEFQISFKTATNTFDSWLN SLWLPPTGFKKL/DNHLKKVYIFPKSFKHNNIDSNGNYNVFSGFTYTDSKLNTNALYDKKYGNN STYNNNNYYNNNNLSNKNNS STYNNNNYYNNNNSNNADKNKTITSTSATILMKENVELYNNGNNNLNNNNLSNKNS EDILKDKSIKWNKYDGYITRTINRILLLACNSMDLLSDESIMMCMVSQQFDFNNVIEK SLDEFNQFAQLDQFULARYEEDVVWKRDYLNHLLETEQSMSIEYLKQQEQSKFVKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (21961. .24357)
/note="GeneID exon scores
173.48 - GSCT_ID dd_00724"
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YTQNYFSTLVGNFEPFSKCKGDELAIIDSFKVYNTSSYFLTFSRSSTNFLGSSSIGHL
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106.68 - GSCJ_ID dd_00725"
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VDQHGKECCVVAHRPPPKCSLRCPPRHECRVNHFGEECCVKVHHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPKHECRINHFGEECCVKSRNDCLTCEDLNCERKG
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TAKCVPSPTTGSSSTSGGHPDPCKDVTCPDGFHCECKDGKTAKCVPSPTTGSSSTSGG
NTNPCSNVNCPDGFYCECKDGKTAKCVPSGPTQPPKPPVCSLRCPPNHECRFNDQGHQ
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TCTYENSCYRNSSNNOVVEVSNNCFNLDGFIKITPTEYSCSDAKIKECALLGKSCSF
QKNSCSNPTSCCPGESICEGLSSGSTSGGGSSGGTSGGSSGGTTSGSSSGGTSGSS
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/db_xref=
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/note="GeneID exon scores (in order of location 0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
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49.4%;
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otein_id="AAS38631.1"
_xref="GI:42733687"
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Pred. No. 0.00014;
0; Mismatches 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 713)
Dechering, K.J., Kaa
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite Plasmodium falciparum Mol. Cell. Biol. 19 (2), 967-978 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 713)
Dechering, K.J., Kaan, A.M., Mbacham, W., Wirth, D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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AF034389
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-NOV-1997) Molecular Biology, University of Nijmegen,
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 TTATTTTTTTTTTTTAT 2829
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                                                       Conservative
                                                                                                                                                                                                                                                            /gene="816"
537. .710
                                                                                                                                                                                                                                                                                       /gene="816"
537. .>713
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/product="sexual stag
/protein_id="AAD12581
/db_xref="GI;3098291"
                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="NF54"
                                                                                                                                                                                                               /gene="816"
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711. .>713
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                                                                                                                              translation="M'
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                                                                                                                                                                                                                                                                                                                                                                                                       organism="Plasmodium falciparum'
                                                                                                                                                                                                                                                                                                                                                             xref="taxon:5833"
                                                                     45.8%;
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                                                    Score 71.2; DB 3;
Pred. No. 0.00045;
0; Mismatches 333;
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                                                                                                                Direct Submission
Submitted (27-JAN-1997) Department
California, San Diego, 9500 Gilman
USA
                                                                                                                                                                                                                                      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 3576)

Escalante, R., Wessels, D., Soll, D.R. and Loomis, W.F.

Chemotaxis to CAMP and slug migration in Dictyosteli

on migh a Bro control
                                                                                                                                                               2 (bases 1 to 3576)
Escalante,R., Wessels,D.,
                                                                                                                                                                                                        97453232
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Mol. Biol. Cell 8 (9), 1763-1775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="AX4"
                                                                                                   Location/Qualifiers
              /sub_strain="AK244"
/db_xref="taxon:44689"
/chromosome="4"
                                                                           organism="Dictyostelium/
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n MigA
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A (migA)
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                                                                                                                        of Biology, University of
Drive, La Jolla, CA 92093
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/gene="migA"
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/gene="migA"
/number=1
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/replace="pbsrl
2900. .2997
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1253^1254
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/note="N-terminus of this protein is similar to other BTI
domain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
U14556 and L16896, respectively"
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TNGEQWTVLKRHTNDPSLNYKYATHSWPVTGCETAFRYFRILQTGKNSNNRNFLVIGG
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bsrl external plasmid, approximately 4 kb"
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Pred. No. 0.00042;
0; Mismatches 243;
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TB domain encoded by GenBank Accession
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                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 149526 bases at least Q40 Consensus quality: 149526 bases at least Q30 Consensus quality: 149526 bases at least Q30 Insert size: 149526; sum-of-contigs Insert size: 149176; 6.5% error; agarose-fp Quality coverage: 12.41x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio (zebrafish)
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BX957346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@eanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:53850295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cyprinidae; Danio.
1 (bases 1 to 149526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-OCT-2004) Wellcome Trust Sanger Institute,
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HTG; HTGS_PHASE2; HTGS_A
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                                                                                                                                                                                                                                                 This sequence will be replaced by the finished sequence as soon as it the accession number will be preserved
                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence.
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rerio clone CH211-117K16,
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                                                      vector_side:right
clone_end:T7
vector_side:left"
                                                                                                    /note="assembly_fragment:03115
clone_end:SP6
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                                                                                                                                                                                           /organism="Danio rerio"
/mol_type="genomic DNA"
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               Length 149526;
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                                                                                                                                                                                                                 Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckes, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Chillingworth, C., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davie, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Gooble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Horneby, T., Holroyd, S., Horrocks, P., Humphray, S., Jagela, K., James, K.D., Johnson, D., Honnard, N., Line, A., Maddison, M., McLean, J., Mooney, P., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., McLean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Scharp, S., Smith, R., Squares, R., Spiares, S., Smith, R., Squares, S., Smith
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Plasmodium falciparum MAL4P1.
AL034557 AL844503
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Plasmodium falciparum
Eukaryota; Alveolata;
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002) 22255708
                                                                                                                                             Barrell, B.G.
                                                                                                                                                                               Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C.
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Hamlin, N., Pain, A., Berriman, B., Hall, N., Bowman, S., Churcher, C., Harris, D., Lawson, D., Quail, M. and Barrell, B.
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                                                                 TTKFVRDANLENADQEYKDYKTTQGPSKQGNDYLKDKCDNKKCSCMEGNVLTDVSSKX
PFGIYAHKYSEKCNCLGAKFVPTWVPPAPPQFPPPALPAPTTFGVNPCEIVNTLF
SDTNKEKDACTLKYGERAPTSWKCI PTGUNTSNEGAATDSEGSDAKSRHKRULAPSGS
NQGSICVPPRRKLYVTPLTKWAEETTKGSKSQESGKAEGTSESGSEAKSRHKRULAPSGS
NQGSICVPPRRKLYVTPLTKWAEETTKGSKSQESGKAEGTSESGSEAKSRHKRULAPSGS
NQGSICVPAPRRKLYVTPLTKWAEETTKGSKSQESGKAEGTSESGSEAKSPGTSSQ
GEKSPQGLSTPASTSSPSNSRDDDLLKAFVESAAVETFFLHHKYYMDKQKELDEKKKQ
QRESGLVGALDGNSGNVDDEDKDPQKKLEKGDIPEFKRQMFYTLGDYRDILVRGGNT
SDSGNTNGSNNNNIVIXEASGDKQDEMKKIQKALDEHINSLKQAASYPNPOQREGQQON
SSLTRETLWKEHAPSIWEGMICALTYKENDEKKIVKDNEVYEKFFGTTFGTTSGKYKE
KXEYNTVKLDENSDTEAADTKATAPSDNTPTELSHFVLREPYFRYLEEWGETFCKERK
KKLAQIKVDCKVDSADYKCSGYGGECKIEDISNGVFADLKCPGGCRECRKYKWIER
KKIEFGEQKSAYVKQKTKCKEESGGGGNGVCGTVKTCDTAAQFLEELGFCKNNDNGEG
KIEFWEQSETFKHTKHCDPCSSFKIDCRNGKCKSGDTKKCKDGITTIDAKEIAKMISS
KIEFWEQSETFKHTKHCDPCSSFKIDCRNGKCKSGDTKKCKDGITTIDAKEIAKMISS
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KYKKFCWGNGGNGEKSATPNATSREKGKKGDOWEKMICYYDENKEKKYGSDAINFCVL
DDGKQHKKEGKKTSYNAFFWKWHDMILHDS VEWRERLINSCINNAKSONCKNIBKCNK
GGCFEKWYKGKKTSYNAFFWKWHDMILHDS VEWRERLINSCINNAKSONCKNIBKCNK
GGCFEKWYKGKKEKWEA KDHFGKQKDIIGCDAGYTLAAVIKLEFLNEDTEEKS
EKGLDAEBAKEIKHLROWLEQAGYRDLAAVGGPCTEGCVAEQNTIMDKFLDEELKEAE
QCKNCFKKRAQDEGFGGARSADSPPAGTEDHPDAEDDDEDDDDDDDEDELKEAE
QCKNCFKKRAQDEGFGGARSADSPPAGTEDHPDAEDDDEDDDDDDDDEDELEEEEE
PGCKTVNDILSTDDRTKQYGDCHEKNYGENGEDWKCGDLTLVDDTKVCWPPPRROCICLY
YIAHESETKNIETODDLRDAFIRTAAAETFLSWQSYKIKNGADKQLDNGTIPEEFIL
RSMYFTYGDYRDICLINTDISKTVNDDAAAKDKJKKFSKDGSKSPSGTTTPDDWWQTY
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EWGEEFCAERGKLEONIGKSCNGINPIQYCSDNRHFCKKACDEKNYVTETKOKEFRAG
EWGEEFCAERGKLEONIGKSCNGINPIQYCSDNRHFCKNKACDEKNYVTETKOKEFRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRWFEEWAEDFCRLRKHKLKDAIKKCRGKNGEEKYCDLNRYDCKVTASGKHVFFEDFDCKDCQYSCAPFVDWIDNQKLEFLKQRKKYTKEITSGGSCGGSGRKKRDATTTNYEEYEKKFYKELKGTKYKVVNNFLEKLNDEDVCTKNNDIKDGGNIDFKNVHSGSAKKGDGNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:23498127"
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KLDDKQIILIRALIKRWLEYFLEDYNKIKHKISDCINNGEGNICKRDCQNKCNCVGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISKKKPQNPPSDTLGGQCTNSKMRSGCEGACAPYRRLHLCHHNLESIETTSKTASDTL
LLEVCMAAKYEGQSINTHYTKHEHSNKDSPSQLCTVLAASFADIGDIVRGKDLFVGNT
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TCEVKSGNNYFRATCGDEKNPSLTSKQCRCDKDKAGKPIKGSGNVNIVPTYFDYVPQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_id="CAD49094.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similar to Plasmodium falciparum variant-specific surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 adfasts scores: E(): 7.8e-149, 43.1% id in 2872 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin(35153. .41725,42757. .44124)
/gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="rep20 Repeats"
join(35153. .41725,42757.
/gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Plasmodium falciparum 3D7"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:36329"
chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002 this sequence version replaced gi:5731897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="MAL4P1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .32958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .44124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or the Malaria Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ייש) (2664 aa)
2 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridge
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KELMIDKPATLGTDIGSDAIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGSYAV

HVWKKZKALBAJIAKAIAEGTNDIAAALBAGKARGEVIKALKGFGURNFFEGICDT

ISSTGNYTKVTEFVNTIYSKYNGTCNLARSSINPTACYTIETELSIKTGGAGTGDHPP

LYAIROMIKGLAEEATEAAKAALAGKAKKKLQYIKLLKE"

ALLIIVLINVIIYLILRYRKKAABAAKAAKLTAAIKEKCTALIBAGFNSSITSINASII

ALLIIVLINVIIYLILRYRKKKAKKKKLQYIKLLKE"

Complement (join (52002...53297,54200...63307))

/gene="VAR"
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QSRLYGELLEKCQSCKKQKCTEGDVDCGKCKAACDFYEDINKWREQWTKIKGKYKT
LYKKATKPGVTTSNNPKDEKDVVDFLKQLLPRKSKNTPGVTAMTPNTLYSSAAGYIHQ
ELGKTYGCNTQKEFCDNKKGKYAFKHPPKEYEBACICDTRQKAQKPIEKKNDCNGIKT
LDRSNGGTGGIDGCNPKIGNYPSWNCERNESKAENKGACVPPRREKFCVSLLAKEGI
                                                                                                                                                                                                                                                        SDDTIVFTNDGKCGHYEGAPFTNLDYVPQFLRWFDEWAEEFCRIRNKLRKIKDACRN
DKERLYCQQNGYDCTTKRIEKGSSCSRENKCITGCSNKCYDYDFHLEKQQNEFKLOKDKY
DKERLYCQSNGYDCTTKRIEKGSSCSRENKCITGCSNKCYDYDFHLEKQQNEFKLOKDKY
DKERLYCGSNGYTPISHSNNYTKKEYYKEFYEELKCYGSYKNFLQLLNNGFYCQEKIEE
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TYPIEIEVLYSDDKQGYUTEKLKDFCRGPNNYNDENLQKWKCYKNGSEYNKCENISWLY
QDPKEYNLHLSVECHSWAKHLLDTITRWEHGLKNCINNFNTVTDCTSKCITKNCECYEA
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ULEKLDVSVIKNGNASHSLLGDULLAAKYEAKNIKELYQQNNSKNGVIDDNDKETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKKTKSTIDLLRVINIPKSDYDIPTKLSPNRYIPYTSGKYRGKRYIYLEGDSGTDSGY
TDHYSDITSGSESEKEMDINDIYAPRAPKYKTLIEVULEPSGNUTTAAGNNTTAAGNNTTAAGNNTTAAGNNTTAAGNNTTAAGNNTTAAGNNTTAAGNNDLY
NTTAAGNNTTAAGKNTPSDTQNDIQSDGIPSSKITDNRWLYTGEEYNYDMSTNSGNNDLY
VPNDYSSGDIPFNTQHNTLYFDKPDEKPFITSIHDRNLYTGEEYNYDMSTNSGNNDLY
NGKNNLYSGQNNVYSGIDFTSNNRGLTSGKHDSYSGIDLINDTLSGNQHIDIYDEVLK
RKENELFGTNHVKHTTINFAKPARDDPLHNQLELFHTWLDRHRNMCEKWNNKEELLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNRFGENAEAYCNSDKIRVTGKKSAGGACAPFRRQNMCDKNLEYLDNTNTDDTDDLLG
NVLVTAKYEGESIVAKHPHKENSEVCTALARSFADIGDIVRGKDMFKRNEEDAVQKGL
RAVFKKINDNLKEKEISDYDNDPNYYKLREDMWTANRDQVWRAITCYIFYYVNYFKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similar to Plasmodium falciparum rifin pfb0030C SWALL:096112 (EMBL:AE001367) (370 aa) fasta sco: 3.4e-65, 53.6% id in 375 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="VAR exon II, could be alternate exon II for upstream VAR gene PFD0005w" complement(join(48479. .49537,49768. .49821))
/gene="RIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_id="CAD49096.1"
/db_xref="GI:23498129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similar to Plasmodium falciparum variant-specific surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 a/fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym: PFD0020c"
complement(join(52002. .53297,54200. .63307))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="1 probable transmembrane helix predicted TMHMM2.0 at aa 328-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(48479. .49537,49768.
/gene="RIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDDIYYDVNDHDTSTVDSNTMDVPSKVQIEMDVNTKLVKEKYPIADVWDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSQLRGDLSRARFHDGLRKAARLGVI PGPANSCDLDHKFYTNI NNGYPPARNPCDLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GOA:Q81218"
/db_xref="UniProt/TrEMBL:Q81218"
/translation="MGTGSSTPSUPKDVKNESHNSARNVLENIGIEIYNEEKKKVNGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKEEWENETHSGNTHPSDSNKTLNTDVSIQIDMDNPKPINQFTNMDINVDTPTMDNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="RIFIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="PFD0010w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="synonym: PFD0015c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="PFD0010w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .46601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fasta scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ý
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gene

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Query Match
Best Local Similarity
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       1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 CAAGATTTAAAAAAATAACCAAAGTAACCTAATCCACTCGAAAGCTATCATGTAATGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGAGAGGAAGAAA 1059
                                                                                                                                                                                                                                                                                    CTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTCAGTATAAAAAGTATTTAACGGAAATATGTAGAATGGAAAAGAAGAATTTGGTATG 335365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTTTATATACATTTTCTT
                                                   TTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTTCAAAAAAATTAGTTTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATTTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATATTATCCTATGATAATAAAGCTATTGTGGAAATTATATTTTATGGAAAATATAATAT 335545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAA
                                                                                             CCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAGGGA
                                                                                                                                              TTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAA
                                                                                                                                                                                                                                        TTTATTTATTTTATATATATATTTTTTTTTTAAATTTTAAATTCATATATTTTAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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GMLCALITHEIDEEKNIKIKSTYSYDQLKKTTNGTTFLEKFARRFQFLEWFTEWSDEFC
REREKKEEVUSKKCKKDHEGCNKPNTKGNHGCVGACKDYEBYISTKKKQNYNTQKEKFD
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KNPGDLSRKDWWNENGPYIWKGMLCSLEKAWGKDTIKNKSNYNYHNYKFSDNRNGFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETFAKRPQFLRWFTEWGDEFCREQKKQLDILKKKCPKETCTNEGKKKECSDACKAYKE
WLQTWKEHYEKQKIKYENDKDSYTNDPDTKQSPQAYQYLNKKLEKICPSGNTSANCEY
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KCMKYPSSQNNNNMPAGLDTPSDYKDTCETCH
RQSLARSADNPSPRAPGGPOPSGYTPDAGGARAETGSPSPQQPPKPPAGNGGVARIL
QPIARVDQDEEEDEDDEEEGGSEEGEGEDVDDSDSSEDENDEEDEDDSHHVDGGH
QEEEPPDETEVVEETVAAPEVKPACEIVKELFNDTNKFKDACNLKYGGNNSRLGWKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNKI DENKELETENESTYCETCESNKVNCNGSGRGTRGKDECTEHNEKGKSWESVENA
NGGNSTEITVEMI DRREELI KNYSKI LEESGNSSDSLEKTSRLEKSVRDQQWECRYKD
EKTDI CKLKNENDKI DLNQYTTEKVELEYWLQDE I EGYY I LKKRKI I EQCKENGGETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWBANGEHI WKGMI YALTYKDNGEKKI VKDNEVYKKLWDBANKKPKETKYQYKNVKLE
BNSGAKFTQP PSPSGONTPTILTNF I SRPD Y RY LEWGSTFCERKKRLEEVPRKECR
GEYPGEKYGGEDGHDCTENGELKHTNNF ADLDCRDCHKQCRKYRKWID IK KFEYYEKGK
DKYQGELDKLNGNSNGNNNCCKE I KKHTSASEFLKELKHCKDGQNSEDDTDKSEEDKK
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GGGTSSQIVGKTASGPNSHPTUSPSSNBRDDGLRDAFIGSAVETFFLWDRYKKLNTK
KPDATLGGLDGIPLAWGAINGYVPSGODNNNGVKLEBGEIPEBEFKROWBYVLGDYBDI
LFGKNDIVIGNTGSGASDKEMKAKEEKIKETIDKVFPNSVSTPPPTPATKPSDEKRKT
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Pred. No. 0.00051;
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ORGANISM
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CQ422641/c
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Best Local Similarity
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    1019 ATTT 1022
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Sequence 767
CQ422641
CQ422641.1
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 7675 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                        TTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAAATAGA
                                                                                                                                                                                                                                                                                                                                   AAAAAAATTTTTTNAAANTNTTTTAAAACCTTNAATNAAANANAATTTTTTNNNTT
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                                                 TTTNAAAAATAATTTTATANTTATNNAANANAAATTTAAAANTNAANANAAAAATTTTA
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                                                                                             TGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCT 1018
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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Pred. No. 0.00071
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BV119878/c
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AUTHORS
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ORGANISM
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VERSION
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BV119878
BV119878.1 G
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PZA01377
                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA amplification
RedTag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bgaut@uci.edu
primer A: TTCTACGTCCAAATGCATCAAAGA
Primer B: AGGAAACCAAGCCTTATGAGAGGA
STS Bize: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR amplification of genomic DNA Template: 50 ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 241)
McMullen,M.D., Vroh Bi,I.,
MPZ-UCI Joint SNP Discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinhaus Hall, Irvine, : (949) 824-2564 : (949) 824-2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CML247 Zea mays
                              /clone_lib="Zea mays CML247"
/dev_stage="seedling"
/note="Organ: leaf; genomic
                                                            /db_xref="taxon:4577"
/clone_lib="Zea mays (
                                                                                         /mol_type="genomic DNA"
/cultivar="CML247"
                                                                                                                         organism="Zea mays"
                                                                                                                                                      ocation/Qualifiers
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CML247
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                               genomic DNA from inbred line"
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Zea mays STS genomic,
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Best Local Similarity
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                                                                                                                       ATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGA 918
                                                  ACTGTTAATTTÄGTTCCAATÄTCCATCACCAÄGGÄTGGATATCCTÄACCGCATÄTCTTGT
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ilarity 61.5%;
Conservative
 14
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Pred. No. 0.00082;
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Search completed: September 16, 2005, 03:01:32 Job time : 4680.65 secs

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Result
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Maximum
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Perfect score:
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                  DB DB
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1: geneseqn1980s:*
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99.7
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ALIGNMENTS

RESULT 1 19-JUN-1998; M645; male; tissue-preferred; plant tissue; differentiated; WPI; 1999-105628/09. Albertsen MC, 30-DEC-1998. WO9859061-A1 Zea mays. Zea mays Ms45 male tissue-preferred regulatory region 08-JUN-1999 AAX07409; AAX07409 standard; DNA; 1394 BP. (PION-) PIONEER HI-BRED INT INC 23-JUN-1997; (first entry) 97US-00880499. Fox TW, 98WO-US012895 Garnaat CW, regulatory region; plant cells; hybrid seed; fertility; ss. Huffman ΩĄ, Kendall Į,

The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably M845), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile New nucleic acid encoding a - useful in mediating plant Claim 3; Page 23-24; 39pp; English. M845 male tissue-preferred regulatory region fertility, especially hybrid seed production

infertile plants

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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the M945 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue-preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably
                                                                                                                                                                                                                               New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.
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                                                                                        ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a

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RESULT 4
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hybrid
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Query Match
Best Local Simi
Matches 1391;
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                                           TTCAAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAATAGAGT
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription
                                                                                                               A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z. mays
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Best Local Similarity
Matches 246; Conserv
The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expension.
                                                                                                                                                                                      A male tissue-preferred regulatory region essential for initiating transcription of
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                                                                                                                                                                                  comprising nucleotide sequences the MS45 gene useful for
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Best Local S
Matches 157
The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                              24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                  14-JAN-2000;
14-MAR-2000;
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2000US-0189167P.
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2000US-0193480P.
2000US-0205230P.
2000US-020534P.
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6.6e-22;
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RESULT 8
ACN85231/c
ID ACN85231 standard; DNA; 96
XX
AC ACN85231;
XY
O2-DEC-2004 (first entry)
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Entry
DT 02-DEC-2004 (first entry)
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Cancer; breast; tumour; cy
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OS Homo sapiens.
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OS Homo sapiens.
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PP US2003099974-A1.
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PP 29-MAY-2003.
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PP 18-JUL-2002; 2002US-001986
XX
18-JUL-2001; 2001US-030622
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    18-JUL-2001; 2001US-0306220P
                                 18-JUL-2002; 2002US-00198846
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237; Conserv
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llarity 39.2%;
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Pred. No. 2.5e-05;
0; Mismatches 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 6381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated polypeptide associated with breast cancer, detecting presence of polypeptide in sample, as a marker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lillie J,
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237; Conserv
   ATTT 1022
                                 TTAAANNTTTNTAANTTATTAAACCAAAATTTTTTTTTAAAAAATTTTTTAAAANTT
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                                                            TGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCT
                                                                                                                                                                                     TTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGA
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Gaps

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RESULT 9
ADR04296
                               The present invention describes an isolated polynucleotide comprising a first, second, third, fourth or fifth nucleotide sequence, or their complement encoding a polypeptide either having flowering locus T gene CC (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also construct comprising the polynucleotide; (3) transforming a cell by transforming a cell with the polynucleotide; (3) transforming a cell by transforming a cell with the polynucleotide; (4) a cell comprising the comprising the comprising transforming transformed plant cell; (5) producing a plant comprising transforming construct; (7) a seed comprising the recombinant DNA construct; (6) a plant comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (8) an construct; (9) an seed comprising a first nucleotide sequence, where the first nucleotide sequence is comprising a first nucleotide, where the construct polynucleotide includes the second, third, fourth, fifth or construct polynucleotide includes the second, third, fourth, fifth or construct polynucleotide includes the second, third, fourth, fifth or constaining a recombinant DNA construct comprising a polypeptide concoded by the polynucleotide comprising isolating the polynucleotide concoded by the polynucleotide comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide sequence (concoded by the polynucleotide comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide sequence concoded by the polynucleotide sequence are repulsed polynucleotide are useful contained to the construct comprision to explant the construct comprision to enhance concoded the construct comprision to enhance construct construct constructs and tissue concoded the construct constructs and tissue construct constructs and tissue constructs and the sequence represents an FT homologue construct.
  Sequence 13400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 63; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danilevskaya O, Her
Rafalski JA, Sakai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3) homologs, useful for floral development, e.g. engineering plant flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-580996/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2003; 2003US-00343477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corn FT homologue nucleotide sequence SEQ ID NO:63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR04296 standard; DNA; 13400 BP
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  BP; 3962 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hermon P, Bruggemann E, Sh
akai H, Cahoon E, Cahoon R,
  2948 C;
  2695
G; 3795 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shirbroun D, R, Klein T;
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Query Match

Score 69.8;

DB 13;

Length 13400

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RESULT 10
AAZ10551
ID AAZ1051
AC AAZ10
AX AAZ10
AAZ
The present sequence represents the P-Ztap promoter of maize. It is used CC in the method of the invention. The specification describes a method for the production of male sterile plants. The method comprises selective expression of DNA encoding a protein that causes tolerance to glyphosate and application of glyphosate. The method uses two DNA molecules, each coperably linked to a separate promoter, whereby the first promoter functions in plant cells to produce a protein that causes tolerance to glyphosate, and the second promoter functions in plant cells to cause the production of a second RNA sequence in a male reproductive tissue. Expression of the DNA promotes tolerance to glyphosate in those tissues in which it is expressed. Expression of the second DNA molecule causes to the production of an RNA sequence which can inhibit the glyphosate commoter for the second DNA molecule which can inhibit the glyphosate commoter for the second DNA molecule which restricts the production of the antisense RNA to only a subset of the tissues which express the first DNA molecule, only the subset of the tissues which express the first DNA molecule, only the subset of the tissues which express the first considered will be susceptible to glyphosate toxicity. In this way, a specific cell type or combination of cell types, depending upon the component of the plant. The methods can be used for production male-sterile plants for use in the production of hybrid seed, for minimizing undesirable crop outcrossing, and for lengthening flower life. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1A-B; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of male sterile plants using tolerance, used for, e.g. production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-551420/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence of the P-Ztap promoter of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-1999
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ches 32;
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RESULT 11
LAXS8751/c
LD AAX587
XX AAX587
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XX Starch
COS Zea ma
FH Key
FT misc_f
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Matches 98
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                                                                                                                                                                 misc_feature
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/note= "functional /
in Claim 15"
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120. .1221
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ln Claim 17"
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in Claim 12"
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                                                                                                                                                                                                                                                                                                                                                         /note= "functional
in Claim 13"
                                                                                                        /note= "functional fragment of cDNA specifically claimed
                                                                                                                                                                                                                                                    1438. .2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "functional
n Claim 14"
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/note= "functional fragment of cDNA specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSII; DU1; dull1 gene; maize; transgenic
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74.2%;
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Pred. No. 0.00015;
0; Mismatches 33;
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waterbinding;

swelling

potential;

gene; ds. DNA encoding

maize Starch synthase III (Dul).

17-FEB-2003

(first entry)

ABX09935 standard; DNA; 6027

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29-MAR-2002; 2002WO-US009574.

10-OCT-2002 WO200279410-A2 **Zea may**ø Starch; starch synthase; glucan association domain; GLASS; linker LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND; granule bound starch synthase; GBSS; morphology; retrogradation;

domain;

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RESULT 12
ABX09935/c
ID ABX099
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                                                                                                                                                                                                                                                                                                                                                    CC This is the nucleotide sequence of the maize gene dull1 (dul). To CC illustrate the role of the dul locus in starch biosynthesis, a transposon CC tagging strategy was used to isolate the gene and describe its CC polypeptide product. The invention reports tagging of the dul locus with CC polypeptide product. The invention reports tagging of the dul locus with CC untransposon, cloning and characterisation of a portion of the gene, and isolation a near full-length cDNA (the present sequence). The amino acid CC sequence (see AAY06199) deduced from this cDNA indicates that Dul codes CC for a 186 kDa protein extremely similar to potato tuber starch synthase CC for a 186 kDa protein extremely similar to potato tuber starch synthase CC endosperm. The Dul product contains unique sequence features in its N-CC terminus that may mediate direct interactions with other starch biosynthetic enzymes. Mutations within the maize SSII gene affect CC totosynthetic enzymes. Mutations within the maize SSII gene affect CC unitains grarch synthase(s), starch branching enzyme (s) and possibly CC containing starch synthase(s), starch branching enzyme (s) and possibly CC containing starch synthase(s). The isolated cDNA can be used to provide an enzyme with which to regulate the production of starch, and with which to produce altered or novel forms of starch, e.g. in transgenic plants. Cx production. Claimed expression vectors comprise the cDNA or fragments of it that code for functional portions of DUI
                                                                                                                                                                                                                                                                                     Query Match
Best Local ?
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                  Sequence 6027 BP; 1800 A; 1177 C; 1441 G; 1609 T; 0 U; 0 Other;
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P-PSDB; AAY06199.
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                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                             TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
                                                                                                       TTAGTTTATTTTTCATTGGAAAAATTGAAATCTCTTGGAAAAATAGAGTTCACATACTAG
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                                                                                                                                                                                                                                                                    Conservative
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77.5%;
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Pred. No. 0.00027
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RESULT 13
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AC ADK12106;
AC ADK12106;
AC ADK12106;
AC ADK12106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated DNA molecule encoding a fusion CC protein consisting of 4 different functional domains selected from glucan CC association domain (GLASS), linker domain (LLNKR), glucosyl transferase CC domain (GLYTR), and C-terminal end (CTEND) which are operably linked to CC one another. The DNA molecule is useful for expressing in plants CC polypeptides including starch synthase enzymes as fusion proteins with CC improved affinity to starch synthase enzymes as fusion proteins with CC compared to plants producing native starch conditied lengths CC as compared to plants producing native starch or starch produced with CC compared to plants producing native starch synthase fusion CC proteins along with granule bound starch synthase fusion CC modified starch having an altered or improved morphology, retrogradation, CC waterbinding, or swelling potential of the granules, gel strength, CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased CC granule size, degree of branching, crystallinity, degree of cross-cCC linking, and increased or decreased glucan chain lengths. This sequence crockes a starch synthase used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 93
                                                                                                                                                                                                   Maize; dull 1; DUI; starch synthase; alpha-1,4-glycosyltransferase cataly
                                                                                                                                                                                                                                                                                        03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                  US2004049810-A1
                                                                                                                                                                                   plant; gene; ss.
                                                                                                                                                                                                                                                    cDNA encoding maize starch synthase,
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                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                      (first
                                                                  /product= "DU1"
                                                                                                   Location/Qualifiers
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77.5%;
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Pred. No. 0.000
0; Mismatches
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                                                                                                                                                                                                     catalytic activity; starch
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                                                                                                                                                                                                                                                       TDQ1.
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                                                                                                                                                                                                   production;
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RESULT 14
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of a maize gene, dull 1 (DUI), and the polypeptide it encodes. The DUI polypeptide has starch synthase activity, and comprises an N-terminal arm region, a C-terminal catalytic region, and a region of about 900 amino acids terminating with the catalytic region. The C-terminal catalytic region has a catalytic domain comprising alpha-1,4-glycosyltransferase catalytic activity. The dul polymucleotide sequence is useful in producing starch e.g. from a transgenic plant or transfected cell. The present sequence encodes maize
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene i
                        (HYAT/)
(MATH/)
(TAON/)
                                                                                                                                                                                                       24-SEP-2001; 2001US-00960352
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                                                                                                                         12-JAN-1999;
11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MYER/) MYERS (JAME/) JAMES
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12-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                  analysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with lactation/muscle/fat deposition
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2000US-00554467
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2000US-00480902.
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G 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                        deposition; genome mapping; gene
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Pred. No. 0.00
0; Mismatches
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0.00027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                identification;
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RESULT 15
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ID AAI872
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DT 06-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC lactation or muscle and fat deposition (designated LMFD), derived from CC cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, (2) appearing as ABX34836-ABX49947, or complements of them. Also included are (2) (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid intended to a promoter and a 3' non- translated sequence that (2) determining a level or pattern of a molecule in a bovine cell or (2) determining a level or pattern of a molecule in a bovine cell or (2) determining (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid molecule obtained from the bovine cell or (2) determining a level or pattern of a molecule in a bovine cell or (3) detecting the level or pattern of the complement or fragment) with a (3) complementary nucleic acid molecule obtained from the bovine cell or (4) tissue, where hybridisation between the marker nucleic acid and the (5) detecting the level or pattern of the complementary nucleic acid is used for (5) detecting the level or pattern of the complementary nucleic acid is used for (5) detecting the level or pattern of a molecule in a bovine cell or the detection of the molecule. The LMFD nucleic acid is used for (5) determining a level or pattern of a molecule in a bovine cell or tissue. (6) tissue useful for genome mapping, gene identification and analysis, cattle breadth of the molecule in a bovine cell or tissue. (7) for genetically improving cattle for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in celectronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 439 BP; 45 A; 51 C; 56 G; 286 T; 0 U; 1 Other;
                      06-NOV-2001
                                                            AAI87279;
                                                                                                 AAI87279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 1009; 245pp; English.
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                      (first entry)
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54.3%;
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Pred. No. 0.
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nes 113;
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Search completed: September 15, Job time: 676.892 secs
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Best Local Sin
Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 346 BP; 188 A; 22 C; 16 G; 120 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US004927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disorders; arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 7339
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DB; AAO07348.
                                                                                                                                                                                                                                                                   334
                           686 CTTACAATAGAGTGATTTTCTTCCGATTTTAT 717
                                                                 154
                                                                                                                                                                                                                                                                                                  446 AGATTTAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAATGTTTAAA
94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; SEQ ID NO 7339; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYSEQ INC
                                                                                                                                                                                                GACTTATATATAATATAAATTTTTTTTTTTTAGAAAATAATTTACATTTAAACAATAAAAA
 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
                                                                   TATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATATCGAAAGGTAAGCTATGACG
                                                                                                                                                                                                                                 GAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAAAT
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                 Score 65.6;
Pred. No. 0.
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63
                                                                                                                                                                                                                                                                                                                                   129;
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92:

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17600, 16997, 156535,

Sequence
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1280, Ap 14164, A 14164, A 2, Appli 22, Appli 2813, Ap 16001, Appli 1, Appli 111, Appli 111, Appli 111, Appli 11, Appli

Sequence Sequence Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1394
1389.2
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Gapop 10.0 , Gapext 1.0
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10817.505 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match Length
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// cgn2_6/ptodata/1/ina/5A_COMB.seq:*

// cgn2_6/ptodata/1/ina/5B_COMB.seq:*

// cgn2_6/ptodata/1/ina/6A_COMB.seq:*

// cgn2_6/ptodata/1/ina/6B_COMB.seq:*

// cgn2_6/ptodata/1/ina/6B_COMB.seq:*

// cgn2_6/ptodata/1/ina/backfTles1.seq:*
      GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
                    BB
                    US-08-880-499-2
US-08-986-542C-1
US-08-968-542C-1
US-09-9554-467A-1
US-09-913-294A-5397
US-09-9806-798B-23
US-09-9806-798B-23
US-09-9806-798B-23
US-09-9806-798B-23
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US-09-9806-798B-23
US-09-9806-798B-23
US-09-9806-533
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US-09-9806-533
US-09-9806-532C-1
US-09-949-016-15348
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US-09-949-016-15349
US-09-949-016-15350
US-09-949-016-15369
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Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 337, Appli
Sequence 337, Appli
Sequence 1357, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 53, Appli
Sequence 15129, A
Sequence 1743, Appli
Sequence 1744, Appli
Sequence 15349, A
Sequence 15349, A
Sequence 15307, A
Sequence 15307, A
Sequence 15307, A
Sequence 15307, A
Sequence 15309, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                              STREET: DOWN CITY: JOHNSTON STATE: IOWA STATE: IOWA COUNTRY: USA ZIP: $0131

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: ISM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Versic PAPLICATION DATA: DATA: APPLICATION DATA: PAPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: BOO ATTORNEY, AGENT INFORMATION: BOO ATTORNEY, AGENT INFORMATION: NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELEPANS: (515) 248-4800
TELEPANS: (515) 248-4800
TELEPANS: (515) 248-4804
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid STRANDENNESS: Single TOPOLOCY: linear
MOLECULE TYPE: DNA (genomic)
US-08-880-499-2
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US-08-880-499-2
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Patent No. 6037523

GENERAL INFORMATION:
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                      Query Match
Best Local Similarity
Matches 1394; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
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3.7 126176
3.8 126176
                      100.0%; Score 1394;
100.0%; Pred. No. 0,
vative 0; Mismatches
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US-09-949-016-15690
US-09-949-016-156535
US-09-949-016-14876
US-09-949-016-14876
US-09-949-016-14164
US-08-451-405A-2
US-09-949-016-16001
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                                                                                                                                   TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
TTOTTORNEY/POOCET NUMBER: 32,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08880499 Patent No. 6037523
Query Match 99.7%;
Best Local Similarity 99.8%;
Matches 1391; Conservative
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APPLICANT: Albertson, Marc C.

APPLICANT: Fox, Tim W.

APPLICANT: Carl, Garnaat W.

APPLICANT: Huffman, Gary A.

APPLICANT: Kendall, Timmy L.

APPLICANT: Kendall, Timmy L.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME

NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
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                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                 TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
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                   TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAGAAATCAGTTTTAAGTCATTGTCCC
                                                                                            GCCAGCCCCATAAATTATTTAAACCGAAACTGAAACTCGAGCGAAACCAAATCTGAGCTAT
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                                                                                                                                            TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG
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TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC
                                                                         GCCAGCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
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COUNTRY: USA
ZIP: 77071

COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0.1 for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968.542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION SOO
PRIOR APPLICATION NUMBER: US/08/968.542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION NUMBER: 35.423
APPLICATION NUMBER: BENJAMIN AATON AGLER, Ph.D., J.D.
RESTENEY/AGENT INFORMATION:
TELEPHONE: (713) 777-6908
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6027 bp
TYPE: mucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: CDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ANTI-SENSE: no
ANTI-SENSE: NO
COUNTY OF THE
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US-08-968-542C-1/c
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TITLE OF INVENTION: dull1 Codes FC
TITLE OF INVENTION: Synthase
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCGregor & Adler, LLE
STREET: 8011 Candle Lane
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CITY: Houston
STATE: TX
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Sequence 3, Application US/08410784A

Patent No. 5912413

GENERAL INFORMATION:
APPLICANT: MYERS, ALAN M.
APPLICANT: JAMES, MARTHA G.
TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE
TITLE OF INVENTION: SUGARY 1

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Weingarten, Schurgin, Gagnebin and Hayes LLP
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/554,467A
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/US98/24225
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 08/062,102
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 1
LENGTH: 6027
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US-09-554-467A-1/c
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; LIBRARY: (gt11
; CLONE: pMgf10; pMg6Aa; pMgt6-2M
US-08-968-542C-1
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Best Local Simi
Matches 93;
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APPLICANT: Myers, Alan M.
APPLICANT: James, Martha G.
APPLICANT: James, Martha G.
TITLE OF INVENTION: dull1 Coding for a No. 6639125el Starch Synthase and Uses
TITLE OF INVENTION: Thereof
FILE REPERENCE: D6036FCT
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Best Local Similarity
Matches 93; Conserv
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77.5%;
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Pred. No. 2.2e-06;
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Pred. No. 2.2e-06;
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OF THE MAIZE GENE
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US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 593827
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Best Local Similarity
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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NAME: Heline, Ph.D., Holliday C
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: ISU-002:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
TELEPHAX: 617-451-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE NO
                                                                 APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H
APPLICANT: Peterson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2523 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410
                  STREET:
CITY: 1
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COUNTRY:
ZIP: 021
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TOPOLOGY: linear
                                                    ADDRESSEE:
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California
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                               E: Knobbe Martens Olson & Bear 620 Newport Center Drive 16th
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Pred. No. 0.00013;
0; Mismatches 39;
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                                              ; NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program;
SEQ ID NO 5397
LENGTH: 279
TYPE: DNA
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                                                                                                                           Sequence 5397, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION UNMERE: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 235-850
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                              ORGANISM: Zea mays
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
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Pred. No. 0.00073;
0; Mismatches 140; Indels
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, NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
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LOCATION: 10, 12, 185-186, 204, 253, 274, 278
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-902-540-1357/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
LENGTH: 612
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Incyte ID No. 6476212 700350078H1
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Local Similarity 69.0%;
les 89; Conservative
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   866 CTTTATA 872
                                                                                                                                                                  686 CTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAAGTCATTTTTATATA
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                                  TGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAATTAGTTTATTTTCT
                                                                                                  AGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTTCTGATTTTTTTAAGAGCTAGTT
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Pred. No. 0.00043;
0; Mismatches 120;
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Pred. No. 0.00029;
0; Mismatches 39
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                                                                                                                                                                                                                                                                                                                                  Length 612;
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320 TATTTTA 314

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RESULT 10
US-08-880-499-2/c
; Sequence 2, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
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US-08-880-499-1/c
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Patent No. 6037523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILLING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. STREET: Box 1000 CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 50131
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                                                                                                                                                                                                                                                                   881 AACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTTCCCAATAAATTACAA 940
                                                                                                                                                                                                                                                                                                                                                                                                                               761 TAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTC
                                                                                                                                             770 CGAGAATCTA 761
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Pred. No. 0.00059;
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                                                                                                                                                                         US-09-806-708B-23
                                                                                                               Sequence 23, Application US/09806708B Patent No. 6784342 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (515) 248-48
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION UNMEER: U$/08/880,499 FILING DATE: CONCURRENTLY HEREWITH
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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TYPE: nucleic acid
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[: USA
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Fox, Tim W.
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ilarity 55.8%;
Conservative
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IER: 0578
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Pred. No. 0.00059;
0; Mismatches 84
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; PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 1055
TYPE: DNA
PREANISM: Artificial sequence
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LOCATION: (1)..(1055)
OTHER INFORMATION: consensus sequence of A.t. and
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                                      AAATCAGTTTTAAGTCATTGTCCCTGAG 1084
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                                                                                                                   ACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATC
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                                                                                 WRTTTATANCGTNNNNNNNNNNAYATTTNTATTTTWWRTRKANNNNNNNAAAYYGAAAW
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844
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xtolk, John A.
TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES ANI
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOPTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-004-056-1/c
US-09-004-056-1/c
; Sequence 1, Application US/09004056A
; Patent No. 6566586
; GENERAL INFORMATION:
; APPLICANT: Calgene LLC
; TITLE OF INVENTION: Plant Expansin Promoter Sequences
                                                                                                                                                                                                                                                                                              RESULT 13
US-09-640-173-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: promoter ; LOCATION: (956) ; OTHER INFORMATION: unknown nucleotide US-09-004-056-1
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CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION UNMBER: 60034914
EARLIER FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                                  Sequence 53, Appl Patent No. 661351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 155; Conserv
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ORGANISM: Gossypium
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Conservative
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Pred. No. 0.00095;
0; Mismatches 128;
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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C o)
US-09-640-173-53
                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows V
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
COMMINISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or
US-09-713-550-53
                                                                                                                                                                                                                                                                                                                     Sequence 53, Application US/09713550

Patent No. 6617109

Patent No. 6617109

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Scolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CAN

FILE REFERENCE: 210121.484C4

CURRENT APPLICATION UMMBER: US/09/713,550

CURRENT FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 205
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Sequence 53, Application US/09825294

Patent No. 6710170

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Fling, Steven P.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CA

TITLE OF INVENTION NUMBER: US/09/825,294

CURRENT APPLICATION NUMBER: US/09/825,294

CURRENT FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 53

LENGTH: 396

TYPE: DNA

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, NAME/KBY: misc feature
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17.1 265
17.1 3114
17.1 156942
US-09-949-016-13779
US-09-949-016-17576
US-09-949-016-11989
US-09-949-016-17130
US-09-949-016-12088
US-09-949-016-13037
US-09-949-016-15039
US-09-949-016-15039
US-09-949-016-15039
US-09-949-016-12740
Sequence 13779, A
Sequence 17576, A
Sequence 39, Appl
Sequence 11989, A
Sequence 17130, A
Sequence 17088, A
Sequence 12088, A
Sequence 13037, A
Sequence 15039, A
Sequence 15040, A
Sequence 15928, A
Sequence 15928, A
Sequence 12740, A
Sequence 12747, Appli
Sequence 1227, Appli
Sequence 12277, Appl
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ALIGNMENTS

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,499

FILING DATE: CONCURRENTLY HEREWITH

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Sweeney, Patricia A.

REGISTRATION NUMBER: 32,733

REFERENCE/DOCKET NUMBER: 0578

TELECOMMUNICATION INFORMATION:

TELEPAX: (515) 248-4800

TELEFPAX: (515) 248-4844

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1394 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-880-499-1
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US-08-880-499-1
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GENERAL INFORMATION:
  Query Match
Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave.,
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08880499
100.0%; Score 157; DB 3;
100.0%; Pred. No. 5.6e-45;
tive 0; Mismatches 0;
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                                            Length 1394;
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                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (515) 248-481
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1:
MOLECULE TYPE:
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APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                    LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Par 1000
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CITY: Johnston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
                                                                                                                                     1155
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121 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                 61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 120
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                                                                                                                                                        1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
                                                         AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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                                                                                                                                                                                                     100.0%; Su
100.0%; Pr
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                                                                                                                                                                                                       Score 157; DB 3;
Pred. No. 5.6e-45;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1081
LENGTH: 1185
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-1081
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; LCCATION: (1)...(385136)
; OTHER INFORMATION: n = A
US-09-949-016-16073
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US-09-543-681A-1081/c
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US-09-949-016-16073/c
US-09-949-016-16073, Application US/09949016
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6605709
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 16073
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/241,755
PRIOR TILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 385136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253848 TCCATTTACTCCCACACACACACACACTTTTTT 253813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081, Application US/09543681A
                                    35 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA 114
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Similarity 57.3%;
CĂACAATTTGTTTTTGTĊCÁCCAGAAÁGACCTAACCCATTTTCTCCCÁAGGACÁTÁTCTÁ 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCCAGATCGCTCCTATTTTGAAATATATAAACGCTTACACACAAAACACACTCATATA 253849
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                                                                                     Conservative
                                                                                                       18.9%;
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                                                                                   Score 29.6; DB Pred. No. 2.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.4; DB 4; Pred. No. 14;
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                                                                                                                            DB 4;
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                                                                                     34;
                                                                                                                              Length 1185;
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CTCCCAAACAATCCATCTTACTCA 118

Mark D. Adams

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US-09-643-990A-1/c
, Sequence 1, Application US/09643990A
; Patent NO. 6528289
, GENERAL INFORMATION:
, APPLICANT: Robert D. Fleischmann
                                                                                              RESULT 6
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US-09-557-884-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-557-884-1
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PATCHI NO. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.6%;
Best Local Similarity 51.5%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION LOTA:

APPLICATION DATA:

APPLICATION ONTA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-195

APPLICATION UMBER: 08/476,102

FILING DATE: JUN-5-195

APPLICATION NUMBER: MS-VI-STORNEY/AGENT INFORMATION:
                                                                                                                                                        677155
                                                                                                                                                                                                                                    677215
                                                                                                                                                                                                                                                                                                              677275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                              132
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                                                                                                                                                        CAACCAACCA 677146
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                                                                                                                                                                                                                                  ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG
                                                                                                                                                                                                                                                                                                          ACTTTAAATTCAGCCTGCTTGCTTGCTATTGCATTTGCATTAAATGCAAGCATAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No. 66
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Sequence 14712, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: URNTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS of INVENTION: USING DISEASE, METHODS OF ILLE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 10-1 2-1 1000 CCC COMPUTER: Dell pentium OPERATING SYSTEM: MS DOS v6.22 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION: CURKOWN'> PRIOR APPLICATION NUMBER: 08/487,429 FILING DATE: 1995-06-07 APPLICATION NUMBER: 08/426,787 FILING DATE: 1995-04-21 ATTORNEY/ACENT INFORMATION: NAME: Kenley K. Hoover CLASSIFICATION NUMBER: 08/426,787 FILING DATE: 1995-04-21 ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                 677155 CAACCAACCA 677146
                                                                                                                                                                                                                                                                                                                                                                    677215
                                                                                                                                                                                                                                                                                                                                                                                                                                                        677275 ACTTTAAATTCAGCCTGCTTGCTTGCTCTATTGCATTTGCATTAAATGCAAGCATAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 40,3
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                         132 CAAACACGCA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                              72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCCAAGCCTTGCCT 71
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Hamilton O. Smith
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Pred. No. 66;
0; Mismatches
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                                                                  ASSOCIATED
OF DETECTION AND
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                                                                  USES THEREOF
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RESULT 9
US-09-949-016-15502
US-09-949-016-15502
Sequence 15502, Application US/09949016
Patent NO. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; ORGANISM: Human
US-09-949-016-14712
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-14713
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14713
LENGTH: 64190
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14712
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PRIOR TILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                          55 TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA 114
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62.5%;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15502
LENGTH: 11022
TYPE: DNA
RESULT 11
US-09-949-016-191201/c
; Sequence 191201, Application US/09949016
; Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 17447
LENGTH: 41815
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/99/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                122
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                                                                                                                                                                                                                                                                     62 AGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 TGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATT 74
                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                  h 17.8%;
Similarity 58.3%;
49; Conservative
                                                                                                                                      ATGTCACATAGAGACATGCATGTA 33141
                                                                                                                                                                                                                             AGACATGCAGATTCACACACACCCGCATAGCTGCTCCTACGGATCCCTGGTCACTCATTC 33117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAACCA 82
                                                                                                                                                                              AACTTCCATGCAAACACGCACATA 145
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63.2%;
                                                                                                                                                                                                                                                                                                                  Score 28; DB 4; Length 41815;
Pred. No. 38;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 4;
Pred. No. 22;
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GENERAL INFORMATION:

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US-09-949-016-14149/c
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US-09-949-016-14149
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US-09-949-016-191201
                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows
SEQ ID NO 14149
LENGTH: 11490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14149, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                            Matches
                                                                                                                                                                                              Query Match
Best Local (
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Best Local (
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SOPTWARE: FRBESEQ for Windows Version 4.0
SEQ ID NO 191201
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR TILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Local Similarity 58.0%;
hes 47; Conservative
    5582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 GTCCTGACGTTGCATGCACACRTGCACGCGCACAAACACACACACACTCTCTCTCATT
                                           98
                                                                                                                          38 CCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACT 116
                                                                                                                                                                         62;
                                                                                                                                                                                                Similarity
                                      CCAPACATCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAA 156
CCTTGCACACCTGATGCCACATCCGCTTGAGTGGCAGGCGAGTGAAGATGTTGCCCCAAA 5524
                                                                                   CAGGGCCTCTGCCTGCCCCTCCCCCCTGCCCCACCACGAGGAAGCCCACGC
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                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                      for Windows Version 4.0
                                                                                                                                                                                         17.7%;
52.1%;
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US-09-710-279-1813/c
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1813, Application US/09710279
Patent NO. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1813
LENGTH: 1413
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Best Local (
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GENERAL INFORMATION:
APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GGTTTTACACACACACACA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 CCATGCAAACACGCACATA 145
                                                                                                                    14
                                                                                                                                                            52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
CAAGAATCGCAATAATATCTTGTAACTCTCTAT
                                      TCTGAACCAAGAGGATACCTACTCCCAAACAAT 106
                                                                                                                    ATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTAT 73
                                                                            ATTGAATTCTACGTGCTCGTTCCACAGTTTGTTTATCTTCATCTGATAATTCATCCATAC 1154
                                                                                                                                                            Conservative
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Pred. No. 29;
0; Mismatches
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Pred. No. 15;
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                                                                                                                                                                                                  Length 1413;
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RESULT 13 US-09-949-016-16740

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US-09-134-001C-1413/c

Sequence 1413, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NO 1413
SEQ ID NO 1413
LENGTH: 1428
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1413
Search completed: September 15, 2005, 08:25:20 Job time: 28.7481 secs
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Best Local Similarity 55.9%;
Matches 52; Conservative C
                                                                                                           1168 CAAGAATCGCAATAATATCTTGTAACTCTCTAT 1136
                                                                                                                                                                                                                      74 TCTGAACCAAGAGGATACCTACTCCCAAACAAT 106
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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20: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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20: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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10230.248 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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_6/ptodata/2/pubpna/US11A NEW PUB.seq:*
_6/ptodata/2/pubpna/US60 NEW PUB.seq:*
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Regult No.	Score	Query Match	Query Query Match Length DB ID	BB	ID	Description
ב	1394	4 100.0	1394	20	US-10-713-381-2	Sequence 2, Appli
N	1389.2	99.7	1394		US-10-713-381-1	Sequence 1, Appli
ω	243.6	17.5	255	20	US-10-713-381-9	Sequence 9, Appli
4	146	10.5	158		US-10-713-381-3	Sequence 3, Appli
u	80.8	5.8	1261		US-10-425-115-134230	Sequence 134230,
0	76.2	5.5	1663	20	US-10-739-930-1857	Sequence 1857, Ap
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-10-425-115-2	-10-425-115-	-425-115-	-10-473-1	-10-425-115-	-10-425-114-	-10-425-114-7	5-115-177	5-114-2	-960-352-100	-10-425-115-415	-10-109-048-11	-10-634-262-1	-10-425-11	-10-425-114-166	-10-425-115-1493	-10-425-114-3088	-10-425-115-1428	-10-425-114-1	-10-425-115-4978	-10-425-115-7531	-10-425-114-2	-10-425-115-4716	-10-425-114-4	-10-425-115-6	-10-343-477A-	-10-198-846-	-10-425-115-5221	-10-425-114-3106	-10-425-115-	4-	0-425-115-14	-10-425-114-	US-10-425-115-51470	5-115-83	4-32	4
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ALIGNMENTS

RESULT 1 US-10-713-381-2

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Sequence 2, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF CURRENT PROFICATION NUMBER: US/10/713,381

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 08/880,499

PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 1394

TYPE DNA

ORGANISM: Zea mays

US-10-713-381-2

Query Match
Best Local Similarity 100.0%; Score 1394; DB 20; Length 1394;

Matches 1394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GENERAL INFORMATION:

APPLICANT: ALBERTSEN, MARC C.

APPLICANT: FOX, TIMOTHY W.

APPLICANT: GARNAAT, CARL W.

APPLICANT: GARNAAT, CARL W.

APPLICANT: HUFFMAN, GARY

APPLICANT: KENDALL, TIMMY L.

TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF

TITLE OF INVENTION: USING SAME

FILE REFERENCE: 578R

CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT FILING DATE: 1097-06-23

PRIOR APPLICATION NUMBER: 06-23

NUMBER OF SEQ ID NOS: 24

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Publication No. US20040221331A1
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION SUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 255
TYPE: DNA
ORGANISM: Zea mays
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Best Local Similarity
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
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US-10-425-115-134230
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Sequence 1857, Application US/10739930

Sequence 1857, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B

FULL REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18
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LENGTH: 1261
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1155 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC-TTGTTCCATCGTC 1213
                                                                                                                                                                                                                                                                                 1119 CCCT 1122
                                                                                                                                                                                                                                                                                                                                                                1059 TTÄGTTTATTTTCTCTTGAGÄÄÄÄTÄGÄÄATCTCTTGGÄÄÄÄATTGGÄGTTGCTÄÄÄCTÄG 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1274 GCAACTTCCATGCAAACACGCACATATGTTTTCCTGAAC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1214 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                                       912
                                                                                                                                                                                                                                                                                                                                                                                                  852 TTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 158
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ilarity 99.4%;
Conservative
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78.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80.8; DB 20;
Pred. No. 2.7e-07;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 146; DB 20;
Pred. No. 5.2e-22;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1261;
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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 23340

LENGTH: 320

TYPE: """
RESULT 8
US-10-425-114-16264
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 1857
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Best Local
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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les 78; Conserv
                                                                                                                                                                                                                                                             Local Similarity
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                                                              182
                                                                                           911 GCCCTAGAAT 920
                                                                                                                            122
                                                                                                                                                         851
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                                                                                                                                                                                                                                                 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
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                                                                                                                                                                                    TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA 121
                                                                                                                                                                                                              TCTTTTTCGTCCACCACCATG
                                                              GCCCTTAATT 191
                                                                                                                            ATTAGTTTATTTTTTTTTTGAGAAAATAGAATTCCCTTGGGAAATTAGAGTTTCTAAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCATTAAAGATCACAACAGCTAGCGTTCTCCCGCTAGCTTCCCTCTCTCCTCTGCCGA
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milarity 73.1%;
Conservative
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ilarity 96.3%;
Conservative
                                                                                                                                                                                                                                              Score 74; DB 18; 1 pred. No. 4.2e-06; 0; Mismatches 35;
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Sequence 16264, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:

APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David APPLICANT: Screen, Steven

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US-10-425-115-141826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 141826
LENGTH: 1326
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Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16264
LENGTH: 624
                                                                                                                                                                                                                                                                                 Query Match 5.2%;
Best Local Similarity 69.1%;
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                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                       1090 TGAAGTTGGTGGTTGTGCTGGTATTTCACCTTTAACTGTAAGGACTAATTTGGGAACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTCAAAAAA 850
                                                                                                                                                                                                                     756 TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCT 815
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TAGGAATCCCTTAGAAAAAAATAGTTTCCAAACTAGCCCTAAAAT 1253
                                         TAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAAT 920
                                                                                    ATTT-TTCCACTGGATTTTCATTTTCCTAAGGAAAATTAGTTCATTTTCCCTTGAGAAAA 1208
                                                                                                                            GTTTCTTTCAAAGAATTTTGATTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAA 875
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                                                                                                                                                                                                                                                              Conservative
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73.1%;
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                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                          Score 73; DB 20;
Pred. No. 1.4e-05;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                     Length 1326;
                                                                                                                                                                                                                                                              Indels
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                                                                                    ; PEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175978C.1
US-10-425-115-83293
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US-10-425-115-83293/c
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                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 83293
LENGTH: 2729
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32493
LENGTH: 2445
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Publication No. US20040034888A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 60.
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 83293, Application US/10425115 Publication No. US20040214272A1
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                                                                                                                                 FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2729)
OTHER INFORMATION: unsure at all n locations
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OTHER INFORMATION: Clone ID: UC-ZMFLB73402B09_FLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         792 TTTAAGAGCTAGTTTGGCAACCCTGTTTCTT-TCAAAGAATTTTTGATTTTTTCAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCTTAATGTTTTTTTTCATGAA 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTAGGGCTAGTTTGAGAACCCTTTTTTTTCCCAAAAGATTTTTCATTTTTCAAAGAAAA 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                       5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.2%;
73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                       Score 72.8; DB 20;
Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.8; DB 18
Pred. No. 2.1e-05;
0; Mismatches 37
    ed. No. 2.2e-05;
Mismatches 87
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                                             Length 2729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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      Indels
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RESULT 13
US-10-425-114-17816/c
US-10-425-114-17816/c
; Sequence 17816, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-425-115-51470/c
US-10-425-115-51470/c
; Sequence 51470, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION ON THE COMMERS US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 51470
LENGTH: 1203
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Best Local Similarity
Matches 102; Conserv
                                                                   APPLICANT:
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NAME/KEY: unsure
LOCATION: (1)..(1203)
OTHER INFORMATION: unsure at all n locations
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ORGANISM: Zea mays
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OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                     Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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76.1%;
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Pred. No. 1.8e-05;
0; Mismatches 31;
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APPLICANT: KOVALIC, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 142853

LENGTH: 1123

TYPE: DNA

ORGANIEM -
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: MRT4577_61761C.1
                                                                                                                                                                                                                                                  y Match 5.2%;
Local Similarity 78.0%;
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702
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                                                                          ARTTAGTTAATTTTCTCTTAGAAAAATAAAATGTCTTGGAAAAATAGAGTTACCAAATT
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                                    AGCCCTA 916
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ACCCCTA 696
                                                                                                                                                       TTTTTAAGAGCTGGTTTGGCAA-CCTCATTTTCTAAGGGATTTCTATTTTACTAAGAAA
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78.0%;
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Pred. No. 2.3e-05;
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                                                                                                                 909
                                                                                                                                                         763
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RESULT 15 US-10-425-114-31957 ; Sequence 31957, Application US/10425114

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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: LIU, Jingdong
APPLICANT: LIU, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Stewen E
APPLICANT: Screen, Stewen E
APPLICANT: Tabaska Jack E
APPLICANT: Screen, Stewen E
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APPLICANT: Screen, Stewen E
APPLICANT: Tabaska Jack E
APPLICANT: Tabaska Jack E
APPLICANT: Cao, Yongwei
TTTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
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CURRENT APPLICATION NUMBER: US/10/425,114
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Result
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Gapop 10.0 , Gapext 1
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CC65693 OGMDQ20TM
CG224225 OGLAGBTC
CG256939 OGMDQ20TV
CC656939 OGMDQ20TV
CC252571 OG4BB05TC
CL235046 ZMMBBb057
CG048704 PUILLO19TB
CG414922 ZMMBBb029
CC439901 PUHRV15TB
CC400575 PUHLU61TB
CC400575 PUHLU61TB
CC400574 PUHLU61TB
CC400574 PUHLU61TB
CC400574 PUHLU61TB
CC400575 PUHSE19TB
CC6082115 PUFDL32TV
CC630219 OGUCG53TV
CC630219 OGUCG53TV
CC630210 OGUCG53TH
CC433618 PUHHP17TD
AL175696 Tetraodon
BZ816381 PUFBA86TD
CL997678 ZMMBH6001
CG2333929 OG0AD14TV
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CG3333929 OGOAD14TU
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5.8	5.8	5. B	5.8	5.8	۶. 8	5. 8	5. 8	5.9	5.9	5.9	5.9		5.9	5.9	5.9	5.9	5.9	5. 9	6.0	0.0
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CC385881	CG254365	CG246849	CC676387	BZ996930	CNS00LT2	CG221693	CC385762	CL984151	CL996481	CC003943	BZ676889	CG071791	BZ778636	CC613918	CC620594	BZ784278	CC435780	CG102092	CC430754	D4/3/3/6
CC385881	CG254365	CG246849	CC676387	BZ996930	AL078714	CG221693	CC385762	CL984151	CL996481	CC003943	BZ676889	CG071791	BZ778636	CC613918	CC620594	B2784278	CC435780	CG102092	CC430754	04/3/3/0
PUHMJ82TD	OGWFU41TH	OGWAL22TH	OGKAS81TH	PUGIR50TB	Drosophil	OGWMG04TH	PUHFK14TD	ZMMBHd000	ZMMBHf000	PUDJN65TD	PUBIG17TD	РИЈВКО2ТВ	ih02f10.g	OGJAG88TV	OGUCC26TV	PUFHV09TD	PUHSN02TD	PUFYW94TD	PUHEPOSTB	LOGDE COTO

ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CC656933 LOCUS S 밁 ORIGIN FEATURES COMMENT DEFINITION Query Match Best Local Sim Matches 961; source Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 93) 1 (bases 1 to 93) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics OGWDQ20TM ZM 0.7 1.5 KB genomic survey sequence. CC656933 CC656933.1 GI:32060225 9712 Medical Center Drive, Tel: 301-838-5843 Fax: 301-838-0208 Unpublished (2002) Other_GSSs: OGWDQ20TV Zea mays Seq primer: TR Class: sheared ends. Email: whitelaw@tigr.org Contact: Cathy Whitelaw Similarity Zea mays primer: TR Conservative /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBMa0554D15" /clone="ZMMBMa0554D15" /clone_lib="ZM,0-7_1.5_KB" /note="Vector: pBCSK; Site_1: HincII; 0.7-1.5 methylation filtered genomic DNA library" 1. .963 Location/Qualifiers Score 948.8; Pred. No. 1.5e 0; Mismatches 0; 963 bp DNA linear GSS 19-JUN-2003 Zea mays genomic clone ZMMBMa0554D15, Rockville, 1.5e-190; DB MD 20850, USA 9; Indels Length 1; Ĕ Gaps 463 60

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E 1 (bases 1 to 915)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Buddman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.M., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OG1AG08TH
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TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMa0716B15"
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Best Local Similarity 98.8%;
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1 (bases 1 to 687)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Malze Genomics

Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville,
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/note="Vector: pBCSK:; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="B73"
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Zea mays
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Consortium for Maize Genomics
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1 (bases 1 to 715)
                                                                                                                                                                                                                                                                                                                                          Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                         Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                        Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
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Similarity 80.1%;
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/db_xref="taxon:4577"
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 CG048704 814 bp
PUILO19TB ZM 0.6 1.0 KB Zea mays
genomic survey sequence.
CG048704
CG048704.1 GI:33920884
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Class: BAC ends
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Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C. Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CL235046 P67 bp DNA ZMMBBb0575001r ZMMBBb (HindIII) Zea mays g ZMMBBb0575001 3', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University
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/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1:
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78.6%;
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Pred. No. 5.9e-09;
0; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                          667
                                                                                                                                                                                                                                                                                                                                                                          892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153;
                                                                                Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 754)

Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 814)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUILO19TD
                                                                                                                              CG414922.1
                                                                                                                                             genomic survey
CG414922
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                                                                                                                                                                                              CG414922
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennetzen, J
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                                                                                                                                                                                                                                                                                                                                          AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCCGATAATCCCCTATCTCATTCTCT
                                                                                                                                                                                                                                                                                                                                                                      AAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTAT 951
                                                                                                                                                                                                                                                                                                                                                                                                        TTCATTCTCACAAGGGAAAAATAGTTTATTTCCCCTTTTGTAAAATGGTAATCACTCGGAA
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/clone lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO;
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/strain="B73"
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                                                                                                                                GI:34505144
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                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88; DB Pred. No. 4.1e.
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                                                                                                                                                                             genomic clone ZMMBBb0290L09 3',
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RESULT 8
CC439901/c
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AUTHORS
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VERSION
KEYWORDS
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JOURNAL
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BACKWARD: M13r
Plate: 0290 row: L
Seg primer: M13r
Class: BAC ends.
                                                                                                                                                                                                                                             CC439901 950 bp
PUHRV15TB ZM 0.6 1.0 KB Zea mays
genomic survey sequence.
CC439901
CC439901.1 GI:30940477
GSS.
                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 950)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                             Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHRV15TD
                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Wing, R.
Sequencing of the maize
Unpublished (2003)
                                                                     Contact: Cathy Whitelaw
                                                                                                                          Bennetzen, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRimers
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ilarity 71.2%;
Conservative
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520 621 9288
              301-838-5843
301-838-0208
                                          Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="ZMMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
/clone="ZMMBBb0290L09"
/lab_host="DH10B"
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/cultivar="B73"
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Pred. No. 4.5e-08;
0; Mismatches 47
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                                          20850,
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AUTHORS
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Query Match
Best Local Similarity
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
Zea mays
                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                      Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHOC67TD
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1 (bases 1 to 652)
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                   Whitelaw, C.A., Quackenbush, J.,
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Similarity 72.4%;
26; Conservative
                                                                                                                                                                                          Class: sheared ends.
                                                                                                                                                                                                        Seq primer: TR
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                                                                                                                                                                                                                                                                                                                                                                                                                Resnick,A., Fraser,C.M., Yuan,Y.,
                                                                                                                                                                                                                           Email: whitelaw@tigr.org
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/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                 Location/Qualifiers
1. .652
                                                                                             /organism="Zea mays"
/mol_type="genomic D
/strain="B73"
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                                                          db_xref="taxon:4577"
clone="ZMMBTa495L13"
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/strain="B73"
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Pred. No. 7.5e
0; Mismatches
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Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA line
genomic clone
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                       EcoRI; 0.6-1.0 kb high
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ZMMBTa495L13,
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6.2**%**; 63.9**%**;

Score Pred.

86.6; DB 8; No. 8.1e-08;

Length

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KEYWORDS
SOURCE
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CC400575/c
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DEFINITION
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                                                                                                                                                                            Query Match
Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                  833
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CC400575
CC400575.1 GI:3
GSS.
Zea mays
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1 (bases 1 to 797)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC400575 797 bp
PUHLU61TD ZM_0.6_1.0_KB Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennetzen, J
TTGATTTTTTCAAAA-AAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAA
                                                                  TGATTTTTTCAAAAAAATTAGTTTATTTTTCTCTTTTATAAAATAGAAAACACTTAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTC
                                                 TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
                                                                                                               TTTAGAGGACGTTGGTAGAGATGGAAAGATATAGAGAAAATAATCTTTTAGAGAATGTTA 518
                                                                                                                                             TTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cathy Whitelaw
                                                                                                                                                                                                                                                      /db xref="taxon:4577"
/clone="ExMMBT8480101"
/clone_11b="ZM_0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
/note="Vected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                           Score 86.6; DB 8;
Pred. No. 8.2e-08;
0; Mismatches 109;
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genomic clone
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                                                                                                                                                                                                         Length 797;
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VERSION
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CC400574
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Best Local S
Matches 163
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                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                           163;
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PUHLU61TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHLU61TD Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 820)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
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CC400574.1
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genomic survey sequence.
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                                                                                                                                                                            TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
AATTATTTGGCCAGCCCCATAAATTATTTAAAC 984
                                                                                                                                                                                                TTCATTCTCACAAGGGAAAAATAGTTTATTTCCCTTTTGTAAAAATGGTAATCACTCGGAA 398
                                                 AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCGATAAATCCCCTATCTCATTCTCT
                                                                              AAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTAT
                                                                                                               TTCATTCTCACAAGGGAAAAATAGTTTATTTCCCTTTTGTAAAAATGGTAATCACTCGGAA
                                                                                                                                   TTGATTTTTTCAAAA-AAAATTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAA
                                                                                                                                                                                                                                            TTTAGAGGACGTTGGTAGAGATGGAAAGATATAGAGAAAATAATCTTTTAGAGAATGTTA
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                                                                                                                                                                                                                                                                        TTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTT
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                                                                                                                                                                                                                                                                                                                                                                                  /clone="ZMMBTa480101"
/clone=11b="ZM 0.6 1.0 KB"
/clone=11be=12M 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                     59.7%;
                                                                                                                                                                                                                                                                                                       Score 86.6; DB 8;
Pred. No. 8.2e-08;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 820 bp DNA linear GSS 19-N Zea mays genomic clone ZMMBTa480L01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20850, USA
                                                                                                                                                                                                                                                                                                                                    Length
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                                                                               951
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                                                                                                               553
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USA

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                   RESULT 13
CG082135/c
LOCUS
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AUTHORS
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CG103452
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ORGANISM
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                                                                                                                VERSION
                                                                                                                                                                  DEFINITION
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                                                                                                                               ACCESSION
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Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                                                                                                                                      909 TAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATT 955
                                                                                                                                                                                                                                                                                                                                              276
                                                                                                                                                                                                                                                                                                                                                                 849 AAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGAGTTGCCAGAC
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                                                                                                                                                                                                                                                                        336
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PUJBELDTB ZM 0.6_1.0_KB Z
genomic survey sequence.
CG103452
CG103452.1 GI:33985746
GSS.
                                                                                        genomic survey (CG082135 CG082135.1 GI: GSS.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                             CG082135 765 bp DNA linear GSS 20-AUG-2003 PUFQX12TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0712B24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize Genomics Consortium Unpublished (2003) Other GSSs: PUJBE19TD Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 471)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                           Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bennetzen, J
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                                                                                                                                                                                                                                                                                                                                             ANATTAGTTCATTTCCTTTGAAAAAATAGGAATCACATGGGGAAATAGTGTTCCCAAAC
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301-838-5843
301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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/clone_TVector:_pCR4-TOPO; Site_1:
/note="Vector:_pCR4-TOPO; Site_1:
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic D
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                                                                                                                GI:33964429
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Pred. No. 1.4e-07;
0; Mismatches 51;
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ZMMBTa0628D13,
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                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 781)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUG53TH
                                                                        9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                      Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey CC630219
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Other_GSSs: PUFQX12TB
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                                                                                                                                            Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                             Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize Genomics Consortium
                                                         Email: whitelaw@tigr.org
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 Location/Qualifiers
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/mol_type="genomic DNA"
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Pred. No. 1.6e-07
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San Miguel,P., Ma,J. and
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Gaps

846

906 197 kb high

ZMMBMa0406J09,

GSS 19-JUN-2003

960

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REFERENCE
AUTHORS
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CG349565/c
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                              Query Match
Best Local Similarity
Matches 125; Conserv
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JOURNAL
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Best Local Similarity 71.8%;
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787 ATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAA 846
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                                                                                                                                                                                                                                                                                                                                        TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 815)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohl
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
CG349565
CG349565.1 GI:34266831
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Other_GSSs: OG0F183TV
Contact: Cathy Whitelaw
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OG0FI83TH ZM_0.7_1.5_KB
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Class: sheared
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ilarity 71.8%;
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                                                                                                                     /db_xref="taxon:4577"
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methylation filtered genomic DNA library"
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/strain="B73"
                                Score 85.2; DB 9;
Pred. No. 1.6e-07;
0; Mismatches 48;
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Pred. No. 1.6e-07;
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Zea mays genomic clone ZMMBMa0705N21,
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                                                                 Length 815;
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                                                         ACTAGECETAAAGTATTTTATAAAATAGAGGAAAAATTEGTETATTTTTCATTG 1
              960
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Search completed: September 16, 2005, 08:08:41 Job time: 4348.69 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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           GenEmbl: *

1: gb_ba: *

2: gb_htg: *

3: gb_in: *

4: gb_om *

5: gb_ov *

6: gb_p; *

8: gb_p; *

10: gb_i: *

11: c
                                                                                                                                                                                                                                                                                                                 4708233 seqs, 24227607955 residues
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14440.280 Million cell updates/sec
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157
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

Result No.	Score	Query Match	Query Match Length	6 B	ID
N	157	100.0	1394	ο .	AX224394
ω	157	100.0	1394	σ	AX224395
4	157	100.0	1394	σ	BD062176
ທ	157	100.0	1394	o	BD062177
6	157	100.0	3343	æ	AF360356
7	146	93.0	158	o	AX224396
ი 8	54	34.4	137327	8	AC135206
ų	50	31.8	50	σ	AX224398
10	40	25.5	40	0	AX224399
c 11	34.8	22.2	174806	N	BX950854
12	34.6	22.0	110127	9	AC104134
13	34.4	21.9	214946	9	AC136896
C 14		21.5	141810	N	CR847532
15	33.8	21.5	214178	ഗ	BX640577
		21.1	117764	9	AC011290
c 17		21.1	162481	J	AC091864
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20.5	20.5	20.5	20.5	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.8	20.8	20.8	20.8	20.8	20.8	20.9	20.9	20.9	20.9	20.9	20.9	
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ALIGNMENTS

RESULT 1 AX224402 AX224402 AX224402 Sequence 9 from Patent WO0160997. Sequence 9 from Patent WO0160997. ACCESSION
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RESULT 3
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Sequence 1 :
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 2 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers
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Sequence 2 from Patent |
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                                                                                                    Similarity
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1 from Patent WO0160997.
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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PD 30-OCT-2001

PD 30-OCT-2001

PD 30-UN-1998 JP 1999504910

PR 23-UN-1997 US 08/880499

PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN, PC C12N15/B2, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC C7K14/34, C12Q1/68, PC A01H5/00

CC Strandedness: Single; CC Topology: Linear; Location/Qualifiers.
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157; Conserv
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1394)
                                                                                                          1394 bp
Male tissue-preferred regulatory
BD062177
                                              Homo sapiens
                                                                             BD062177.1 GI:22607782 JP 2001520523-A/2.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1394)
Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A.
Kendall, T.L.
                                                             Homo sapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.9e-40;
D; Mismatches 0;
              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Local Similarity 100.0%; Pred. No. 1.9e-40;
hes 157; Conservative 0; Mismatches 0;
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                                                                                                                               Direct Submission
Submitted (11-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
                                                                                                                                                                                                                                                                                                                                      AF360356
Zea mays male fertility
AF360356
AF360356.1 GI:14028756
                                                                                                                                                                              2 (bases 1 to 3343)
Fox, T.W., Trimnell, M.R.
                                                                                                                                                                                                                    Fox, T.W., Trimnell,
Cloning of M845, a
                                                                                                                                                                                                                                                           clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
                                                                                                                                                                                                         Unpublished
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23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
/gene="M845"
join(<1392. .1768,1898.
                          <1392. .>2942
                                     /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                  Male tissue-preferred regulatory region and Patent: WO 0160997-A 3 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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/product="male !
join(1392. .1768
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                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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RIMRYMLEGPRAGEVEVFANLPGFPDNVRSNGRGQFMVAIDCCRTPAQEVFAKRPMLR
TLYFKFPLSLKVLTMKAARRMHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK
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DYRPVKHELAPYGEVMGSWPRONASRLRFGRLEFVGEVFGPESIEFDLCGGPLFPYAGLA
DGRVVRMMGEAGWETFA VMQPDWSEEVCAMCVNSTTRAVHEKEEFCGRPLGLEFHGE
TGELYVADAYYGLMVVGQSGGVASSVAREADGDPIRFANDLDVHRNGSVFFTDTSMRY
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join(1392. .1768,1898. .2182,2280.
/gene="M845"
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/product="male fertility
/protein_id="AAK52489.1"
/db_xref="GI:14028757"
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Pred. No. 7.2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-APR-2003) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA Olymbra 11, 2003 this sequence version replaced gi:24635891.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality y-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32874 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69957-70761, 89355-90416, 99951-99009,
                                                                                                                                                                                                                                                                                                                                                    105316-105607, and 133052-133152 are covered by Monsanto only. Th nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-OCT-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA 3 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J., Collura,K. and Thompson,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Curri
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5 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T.,
Saski,C., Henry,D., Thompson,S., Simmons,J., Thurmond,S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-JAN-2003) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA
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Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC135206
AC135206.3 GI:27596977
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Collura, K. and Thompson, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Currie, J., Collura, K. and Thompson, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arizona,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   izona, 303 Forbes, Tucson, (bases 1 to 137327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 137327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
/note="unknown protein" complement(join(638. .838,1141. .1276,3132. .3244,3326. .342 3513. .3727,3812. .3934,4024. .4054,4157. .4216,5088. .5243,
                                                                                                             /note="(japonica cultivar-group)"
complement(638. .9495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (06-NOV-2002) Arizona Genomics Institute, 303 Forbes, Tucson, AZ 85721, USA
                                                                                 /gene="0J1041F02.
                                                                                                                                                                                               /db_xref="taxon:39947"
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                                                                                                                                                                      /clone="OJ1041F02"
                                                                                                                                                                                                                                                                                                          .137327
                                                                                                                                                                                                                                                                           (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear PLN 16-APR-2003 chromosome 3 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rambo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , T : ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Currie, J. and
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SG

translation="MGPPAAPPSPSSSSGGSSRRRRLERRNAAKHIGYDASNFCAYP

SGS

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repeat_region
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QPILLKCLQDEASSRVRIAALKAVGSFIEYNDGGDVVKIRDFVPSILAVSRQCLAN
GEBUVAS IAFEIFDELIESPAPLLGDSVRSIVQFSLEVCSNQELEINIRQQAIQIISW
LVKFKASFLKKHKLVIPILQVWCPLLTETADEOGDSDLAADRSAABVIDTWAINLPRH
LVKPPVLEFASVSFRHINPKYRBAAVTSLGVVSSGCCEHLKOKLEDCLKVVLEALKOQE
QWVRGAASFALGQFAEHLQPSILSHYESVLPCILAALEDPSDEVKEKSYYALAAFCED
MGENILPYLDPLWCRLVMSLQGSPRNLQETCWSAIGSVAAAABQAFMYAEKVLEWMK
GEWILFYLDPLWCRLVMSLQGSPRNLQETCWSAIGSVAAAABQAFMYAEKVLEWMK
GFWVLTNDEDLCARARATEVVGIVAMAVGRARMETILPPFIEAAISGFVLDYSELREY
THGFFSNVABILDDSFAQYLHVVPILAFSCNLDDGSAVIDDDASVDNGFSGVSSDD
DVNDEPRVRUNISWITIIADILTAIRAIPPAHADVLEKQKDILDTWATKLBUD
DVNDEPRVRUNISWITIIADILTAIRAIPPAHADVLEKQKSPHPPQDKTMVVATLAEV
KEVVAQACTSLADIVAGSYEDPIFTKLFDSIMKFAKSPHPPQDKTMVVATLAEV
NOOMAA BOLAVUTUVATLAEVIT
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complement (join (26563. .26772,27082. .27288,27430. .2753

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28790. .28874,29560. .30575))
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TTNDKGKGLHIEDDAGETDNPKDAVDSVTKQISGIAISESLVVATSSTDATNNSKSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQGMGAPISAYVDKIMPLVLKELASSEATNRRNAAFCVGEMCKNGGAAALKYYGDILH
GLHRLFADSEPDDAVRDNAAGAIARMIMVQPQSIPLNQILPLVPDVINAFAQVVVSPN
ESDEVKTVVAKAVSHLISVYGQQMQPILSALPPAHANALASFANRR"
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/gene="0J1041F02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unknown protein"
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/gene="OJ1041F02.2"
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RTAKTPNVRQLAAVLLRKKITSHWPKLPPHAKASLKQALIDSITIDHSHLVRRASANV
                                                     codon_start=1
'product="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="putative transposon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="putative MITE, Gaijin/Gaigin-like"
protein_id="AAP06847.1"
db_xref="GI:29893593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="0J1041F02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAP06844.1"
| db_xref="GI:29893590"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="unknown protein"
                                                                                                                gene="0J1041F02.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .19454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .22206,23772. .23996,24523. .24660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTA,
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CDS

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Query Match
Best Local S
Matches 60
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119439
                                                                                                                                              119499
                                                                         124
                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                 60;
                                                                                                                                                                                                                                                                                                                      Similarity
   CCTCCATGCA 119430
                                                                     CTTCCATGCA 133
                                                                                                                                          CCTTGGCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACGCTGACTCATGCAA 119440
                                                                                                                                                                                             CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 123
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGKKGHPFFASRKIHKGAGQDILAVEDEDMDSICAFERDPPLCPYHVLYELEVTMPIH
WSNKWIJADKSFLGTSTTEQNSAEHADPGKHLANFHDKOKKSKESSODVIDVIDDECLI
ASSSCFHASIFESKQHERVQHELPEVTPKGCQTANLHTDKYRFETAAQVCGNSKHVKF
LNEWLKGWDERCHRKQNIVTNOSMNGBSCQDGSDTDYSEDASDYENVLLITGPVGCG
KSAAVFACAREQGFNVIELNPRKTVVFPFLPHNKLLAQTLDLKEDKTHDSSHPSIKYI
PTRVFVHMNRNSIISISAHSSSLSVIKLHCLINTSDHRNGAYVRQKFEEATKSHGLEK
WSQEEIIGLPISNSLDPASGTPGTAEYKQVINKTLILFEDVDTVPDEDGRGTISTILKM
VETTKWPIHLTSNKKDPPLPHLLAQLVLDFTYPSSAELLSHUDMICKSEGVEITVPQQ
KHIIDAFLGRLKKCLSCPSLLDLAVHSTVPRIMPWDFCKLSETIYMEIDKTIVTAE
QKKKQMEVSEFEGLELQIMTPLITKGRSAGKTRKEKKSKLKHGRSADCUDASPCKNDLD
DFHDSPDIFLESNHQRMRNRRGVVLFAESDDDLADAHAAKDATFTVQEGRLLPQSSEL
PCLYGHGISNIVPESVEFEQQSVPHLHEBVISNGLFFDSSRAFEFASSFQNQLESNM
PGS15QICTOTFWSQGISCVPESSFMVGGTSASISSDDLLSCLNARDHASCSITGYQLMDECS
RAESWWLLSGKKNNDSCKVEHYQDTWARLRQCHPVLPCDRNHNRSVSGALKRVSRYSD
RAESWWLLSGKKNNDSCKVEHYQDTWARLRQCHPVLPCDRNHNRSVSGALKRVSRYSD
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RAESWRLSGKKNNDSCKVEHYQDTWARLRQCHPVLPCDRNHNRSVSGALKRVSRYSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein"

/complement(join(35049. .35184,35866. .36033,36922. .37205,

37280. .38523,40038. .40104,40196. .40287,40406. .40617,

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41678. .41760,42229. .42259,42907. .43088,43594. .43753,

44229. .44426,44622. .44676,45877. .45992,46149. .46313,

46447. .46620,47271. .47470,47915. .48019,48200. .48263,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative MITE, MITE-adh, type G-like" 51474. .51836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative MITE, MITE-adh, type M-like"
39681. .39879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBESDLMLISCHPESNDISDPSLTPYTESDORFSYSKOLEMGSIYAQHGLCIFLQDSQ
ATDDGFVDFLQELLFSGTTTTSLGKFVSSGISCGDGSGNISHVKYPTSCISKREBQA
RLREVLLPVVPPKLSQSLRGPAFVDVLSSMSQISQLENMQLSECKASSKQRRCRQPRH
YLSGGALSLSAEDIGLLAQCSTFSDRRESETIIEQAIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGPPKAGGGGEAGGAGLPPLAAGDGTPEKVKKRGRPRKSEAGKKPSSNRETTGLEQD
SKDEVILVDESPQKKQRKGRGKNQGAALKVPNRKHCKALESTDGHESCQQLRSSQTQA
VLPQKSPTSVDIDLVTGPSEASPVNDNVDALDNEDKPQLIVDLRSEANIAAEENRRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative MITE, MITE-adh, type D-like"
complement (31668: .31815)
complement (35049. 49855)
/gene="OJ1041F02.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HANGSVKLADFGLAKEITKFNVLKSCKGTVYMMAPEVVNPKTTYGPEADIWSLGCTVL
EMLTRQLPYPGLEWTQALYRIGKGEPPAIPNCLSRDARDFISQCVKPNPQDRPSAAKL
LEHPPVNRSMRSIRSMRTSSRSNSSILVLLIMMSWPGRTIRYREAILSTAQSSTPTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSEEFTGTSSLSTTNDDETSSTTTESMFYISPNGRFRRKIRSMNRGMLLGSGSFGTVF
EGISDEGVFFAVKEVCLCDQGSNAQQCIFQLEQEIALLSQFEHENIVQYYGTDKEDSK
LYIFLELVTQGSLASLYQKYRLRDTHVSAYTRQILNGLTYLHERNIVHRDIKCANILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSPPAASAPASGSPSLACSPACSLDLTSFRIGGSGDGCRDVQLLCSSLGLSGVDDFAV
PVADWEAHKAGRSSFSSASTFRFREESPFALDSFVREVAASEPFSLEAPAAAFVLP
AKETPRSVALEAPAPLLRVDFWEPARFDVRKASGEGGIKGVRPPPVVLKPPPESWVRPA
VCVVESTWDILRSFAPEEDSHAHAPASRSGGDSACQDAGEEEDDAAAVLTLEELRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MGGSADPEAPTPTPSPSPSPAKATPSPASADGNRLRRCVQSKLS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="0J1041F02.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                               34.4%;
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                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                          Score 54; DB 8; Le
Pred. No. 1.4e-06;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                            Length 137327;
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                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                             /organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/mol_type="unassigned
/db_xref="taxon:4577"
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from Patent WO0160997.
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100.0%; Pr
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100.0%; Pred. No. 0.0
ive 0; Mismatches
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                                        174806 bp
CH211-125M22,
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                                        DNA linear HTG WORKING DRAFT SEQUENCE,
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 172622 bases at least Q40
Consensus quality: 173174 bases at least Q30
Consensus quality: 173717 bases at least Q20
Insert size: 174406; sum-of-contigs
Insert size: 182163; 2.3% error; agarose-fp
Quality coverage: 11.29x in Q20 bases; sum-of-contigs Quality
Coverage: 11.03x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
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1 (bases 1 to 174806)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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74721
133369
133469
150794
150894
172652
                                                                                                                                                                                               fragment church
                                                                  /note="assembly fragment:00366
fragment_chain:1"
172752. .174806
                                                                                                                                                                                                                                                                                                  vector_side:left"
                                                                                                                                                                                                                                                                                                                                    clone_end:SP6
                                                                                                                                    /note="assembly_fragment:00028
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fragment_chain:l"
                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:02018
fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-125M22"
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74720: gap of 100 bp
13368: contig of 58648 bp in length
13468: gap of 100 bp
150793: contig of 17325 bp in length
150893: gap of 100 bp
172651: contig of 21758 bp in length
172751: gap of 100 bp
172651: gap of 100 bp
174806: contig of 2055 bp in length.
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                                                                                                                    Submitted (20-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 20, 2002 this sequence version replaced gi:18677630.
                                                                                                                                                                                                                                             Direct Submission
Submitted (15-FEB-2002) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (04-DEC-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 110127)
Tomlinson,C., Haakenson,W. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-525L16
Unpublished (2001)
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Homo sapiens BAC clone RP11-525L16 from 2,
AC104134
                                                                                                                                                                             Direct Submission
                                                                                                                                                                                             Waterston, R.
                                                                                                                                                                                                                                MO 63108, USA
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Sulston, J.E. and Waterston, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                   63108, USA
(bases 1 to 110127)
                                                                                                                                                                                                              (bases 1 to 110127)
Center project name: H_NH0525L16
                Contact: sapiens@watson.wustl.edu
                                                   Web site: http://genome.wustl.edu/gsc
                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                        Louis,
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                                                                                                                                            USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-554H10, 2000 bp overlap;
the clone sequenced to the right is RP11-450E9, 2000 bp overlap.
Actual start of this clone is at base position 151996 of
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4669. .4846
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999. .. 1297
                     /rpt_family="Alu"
9005. .9219
                                                                                    /rpt_family="L2"
8585. .8756
                                                                                                                          /rpt_family="Alu"
8537. .8577
                                                                                                                                                          7953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLone
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 rpt_family="L2"
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                                                                                                    /rpt_family="AT_rich"
20887. .21186
                                   /note="match to EST BG571642 (NID:g13579295)"
21357 .21652
                                                                                                                                        /rpt_family="L1" 20737. .20769
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9849. .9976
/rpt_family="Alu"
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15439. .15440
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18057. .18074
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14391. .14655
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9890. .20198
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18075. .18379
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17995. .18056
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17384. .17534
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|6889. .17116
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6533...16747
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.5837. .15915
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5731. .15824
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2314. .12607
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11362. .11476
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| 1215. .11264
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10483. .10759
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KEYWORDS
SOURCE
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AUTHORS
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
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Best Local
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                        Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B.,
Graham, L., Karade, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connot, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phuhkhang, P., Pierre, N.,
Deachnyka A., Pamaram, T., Pamaram, P., Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Charga, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., Chargaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Mellean, C., Micol, R., Norbu, C., Mathews, C., McCarthy, M., Mellean, C., Nicol, R., Norbu, C., Minews, C., McCarthy, M., Mellerin, J., Meneus, L., Mihova, T., Menen, C., Horton, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phinkhang, P., Pierre, N., Raymond, C., Retta, R., Peterson, K., Phinkhang, P., Pierre, N., Raymond, C., Retta, R., Schauer, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Winson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Homo sapiens chromosome 15, clone RPI1-86001, complete sequence.
AC136896
AC136896.6 GI:29135656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 214946)
Birren,B., Nusbaum,C. and Lander,E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Cooke, P., Corum, B., DeArellano, J., Hagos, B., Hagos, B., DeArellano, J., Galegan, J., Hagos, B., Hagos, B., Warghan, J., Sarada, A., Kalas, C., Liev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manthews, C., McCarthy, M., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Mahova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassilie, H., Venkataraman, V.S., Viel, R., Vo, A., and Zodv, M., Whan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zodv, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-MAR 2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 21, 2003 this sequence version replaced gi:27877278. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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------- Project Information
Center project name: L27824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35805 ATCCAACATACTAAGAAAAGAAGGTAGCTTTCTTAACCCCAATAAATGTAACCTATGAAAA 35864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35745 TCATCTCTATGGGCAGAAAAATCATTTGACAAAATTACGCATTCTTCCATGATGTAAAC
                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 13909 bases at least Q40
Consensus quality: 140415 bases at least Q30
Consensus quality: 140735 bases at least Q20
Insert size: 141110; sum-of-contigs
Insert size: 1416600; 2.5% error; agarose-fp
Quality coverage: 8.52x in Q20 bases; sum-of-configs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 TTCC 128
                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 3, 2004 this sequence version replaced gi:53145936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McLay, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Exctinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 141810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR847532 141810 bp Danio rerio clone DKEYP-86C9, ***
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                                                                                                                                                                                                                                                                                                                                        coverage: 8.64x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: zKp86C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CR847532
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                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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46870
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/rpt_family="MLT1D"
complement(38856. .39656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.9%; Score 34.4; D; 54.8%; Pred. No. 3.7; tive 0; Mismatches
             19172: contig of 19172 bp in length
19272: gap of 100 bp
46769: contig of 27497 bp in length
46869: gap of 100 bp
52415: contig of 5546 bp in length
52515: gap of 100 bp
100 bp
of 5546 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA linear HTG 03-OCT-2004 SEQUENCING IN PROGRESS ***, 8
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                        41846 ACAGTGACCCCTACATCCTTGTGCCTCAATGCATATTGTACAAGTGTACAGAGGTTGGGT
                                                                                                                                                                                                                                                             132 CAAACACGCACATATGTTTCC
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                                                                                                                                                                                                                                                                                                                                                         12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                      BX640577.17
HTG.
                                                                                                                                                        Zebrafish DNA sequence from
Direct Submission
              McGuire,S.
                                                                             Danio rerio
                                                                                       Danio rerio (zebrafish)
                                                                                                                                           complete sequence.
                                                                                                                                                                      BX640577
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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19273. .4
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131433. .141810
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fragment_chain:1"
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fragment_chain:1"
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/clone="DKEYP-86C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="assembly_fragment:01302
!ragment_chain:2"
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:ragment_chain:2"
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ragment_chain:1"
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fragment_chain:1"
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52.5%;
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DKEY-117014 in linkage
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ikage group 14,
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Search completed: September Job time: 528.823 secs

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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest cond mality representation will be here
58421
                                                                                                                                                                                                                                      58301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-117014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery system (Zhirong Bao and Sean Eddy, submitted), and thosbeginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this is found the longest good quality representation will be
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Contact: zfish-help@sanger.ac.uk
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TCAAAAAAAACTTATTAGTCC
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                                                        CAAACACGCACATATGTTTCC
                                                                                                                      ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
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/mol type="genomic DNA"
/db xref="taxon:7955"
/clone="DKEY-117014"
/clone_lib="DanioKey"
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Pred. No. 5
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Post-processing: Minimum Match 0%
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12227.321 Million cell updates/sec
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157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqn2001as:*
geneseqn2001bs:*
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and is derived Pred. No. score grea No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

18 20	C 1154 12	0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result
30.2 30.2 30		157 157 157 157 157 146 50 31.4	score
19.2 19.2 19.1	19.5 19.5 19.5 19.2	100.0 100.0 100.0 100.0 93.0 31.8 25.5 20.6	Query Match
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ADB08983 ADB12064_07 AAH76335	AAF22279 ADA02717 ADB72455 ADE95965 ADE95965 ADP67076 ADAA51436	AAH76340 AAX07408 AAX07409 AAH76332 AAH76333 AAH76334 AAH76336 AAH76337 AAH76337 AAH76337 AAH76337 AAH76337 AAH76337 AAH76337 AAH76337	SUMMARIES
Adb08983 Alloiococ Continuation (8 of Aah76335 Z. mays M	Aaf22279 BAC conta Ada02717 Mouse Nfa Adb72455 Mouse Nfa Ade95965 Mouse Nfa Adp67076 Human mit Aaa51436 A. thalia	Aah76340 Z. mays M Aax07408 Zea mays Aax07409 Zea mays Aah76332 Z. mays M Aah76333 Z. mays M Aah76334 Z. mays M Aah76336 Z. mays M Aah76337 Z. mays M Aah76337 Z. mays M Aah76337 J. mouse ato Aca48402 Prokaryot Abn80329 Human Che	Description

The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male feertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays M845 promoter fragment

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of.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

Example 5; Fig 8; 50pp; English.

;	45	44	43	42	41		c 39			c 36	35	c 34	33	32	c 31	c 30	29		c 27				c 23	22	c 21
	28.4	28.4	28.4	28.4	28.4	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.8	29.2	29.2	29.4	29.6	29.8	30	30
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	AD084654	ADQ85536	ADQ86652	ABA00762	AAF15843	ADB92108	ADB96917	ADB87934	ADB20845	ACF62730	ABD32806_5	ACN45162	ABN67847	ADD71973	AAS32893	AAS32892	ADS57339	ADA68284	AAT42063_06	AAL62902	AAF22303_2	ADF00796	AAH13328	ADD33404	ADD33403
	Human	Adq85536 Human tum	Adq86652 Human tum	Aba00762 P5CR rela	Aaf15843 Human pro	Adb92108 Human MDR	Adb96917 Human MDR	Adb87934 Human UGT	Adb20845 MRP1 base	Acf62730 Cancer ba	Continuation (6 of	Acn45162 Human gen	Abn67847 Streptoco	Add71973 Human uri	Aas32893 Human gen	Aas32892 Human gen	Ads57339 Bacterial	Ada68284 Arabidops	Continuation (7 of	Aal62902 Vernonia	Continuation (3 of	Adf00796 Bacterial	Aah13328 Human cDN	Add33404 Mouse mit	Add33403 Mouse mit

ALIGNMENTS

AAH76340 standard; DNA; 255

BP.

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RESULT 1
AAH763400
ID AAH77
XX AAH77
XX AAH77
XX XX XX
DE Z. n XX
XX Zea
DX Zea
XX Zea
PN W020
PN W020
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PR 17-F
PR 17-
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                                                                                                                                                                                                     Sequence 1394 BP; 411 A; 311 C;
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ilarity 100.0%;
Conservative
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Pred. No. 2.1e-42;
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Pred. No. 1.3e-42;
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                                                                                                                                                                                                                 Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.
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tissue; differentiated; hybrid seed; fertility; ss.
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CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                        AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                         AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                               CGTGTCATCTCACATGCCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
                                                                                                                 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
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                                                                                                                                                      Score 157; DB 2;
Pred. No. 2.1e-42;
); Mismatches 0;
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                                                                                                                                                                                   Length 1394;
                                                                                                                                                         Indels
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1275

CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311

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RESULT 4
ANAPGA32
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RESULT 5
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the plant and each sis also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.

    mays Ms45 male tissue-preferred regulatory region encoding

                                                       29-OCT-2001
                                                                                                                                                                 AAH76333 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue preferred regulatory region from Z.
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                                                                                                                                                                                                                                                                                                                                           CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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                                                                                                                                                                 DNA;
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Pred. No. 2.1e-42;
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Best Local 9
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hybrid
                                                                                                                  Z. mays Ms45 male
                                                                                                                                           29-OCT-2001
                                                                                                                                                                     AAH76334;
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                        WO200160997-A2
                                                                            hybrid seed;
                                                                                         M845; male tissue;
                                                                                                                                                                                                AAH76334 standard;
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d seed; ds.
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                                                                                                                 tissue-preferred regulatory region
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                                                                                                                                                                                                DNA;
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                                                                                                                                           entry)
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                                                                                         male fertility;
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Matches 157
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                                                                                                                                                                                                                                                                                                                                                  hybrid seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                     mays Ms45 male tissue-preferred regulatory region fragment
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Pred. No. 5.4e-39;
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Best Local :
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     The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the M945 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The
                                                                                                                                                                                                                                                                                  A male tissue-preferred regulatory region essential for initiating transcription of
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                                                                                                                                                                                                           Claim 14; Page 32; 50pp; English.
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hvbrid seed; ds.
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                                                                                                                                                                             The invention relates to detecting atopic dermatitis or psoriasis comprising assaying the levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis, comparing these levels with those of a healthy person, and determining that if the levels of indicators are higher or lower, then this indicates the disease. Also included are a reagent for detecting atopic dermatitis or psoriasis, a kit for screening for treatments, a transgenic non human vertebrate animal models for the diseases, an agent for inducing the diseases in mice and a DNA chip for assaying for the indicator genes. The method is used for treatment, detection and animal models for research of atopic dermatitis and psoriasis. The present sequence is a Mouse atopic-dermatitis/psoriasis-associated EST
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Z. mays
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14-MAY-2003; 2003JP-00136544.
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anti-inflammatory;
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                                                                                                                                                          (expressed sequence tag).
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ni K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 14
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                                                                                                        BP; 1029 A; 658 C; 590 G; 990 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA; 3267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinagawa
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                        20.6%;
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Score 32.4; D. Pred. No. 2.2; O; Mismatches
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Pred. No.
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                        2.2;
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                                                 DB 12;
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  56;
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        the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of identifying a for cellular proliferation; (8) cellular proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation—required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent
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Wall
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06-SEP-2001; 2001US-00948993

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-00072851

06-MAR-2002; 2002US-0362699P
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                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACA48402 standard; DNA; 2352 BP
                                                                                                                                                                                                                                                                                                                                                  Claim 14; SEQ ID NO 36272; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
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RESULT 11
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The invention relates to a nucleic acid (I) comprising a sequence a least 18 bases in length of a segment of chemically pretreated DNA of genes associated with development selected from 87 genes listed specification such as ACCDN, ADFN, or AFD1 and comprising one of 35 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with
                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heart disease; epilepsy; histone deacetyladwarfism; single nucleotide polymorphism;
                                                                                                                                                                              associated with
                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP007536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antidiabetic;
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                                                                                                                                                            nucleic acid useful for diagnosis and therapy of diseases iated with development genes such as diabetes, comprises a segment of chemically pretreated DNA of genes associated w.
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                              Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve a construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                      01-APR-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF22279 standard;
                                                                                                                                                                                                                                              13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                           17-MAR-2000; 2000WO-US007392
                                                                                                                                                                                                                                                                                                                                                                            WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAC containing repeats from centromeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF22279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15734 BP;
                                                                                                                                                                                                                                  16-DEC-1999;
                                                                                                                                                                                                                                                                                                 18-MAR-1999;
                                                                                                                                                                                                         (UYCH-)
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                                                                                                                                                                                                        VIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATC
                                                                         Page
                                                                                                                                                                             Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                              michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                         CHICAGO
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                                                                                                                                                                                                                               99US-0153584P.
99US-0154603P.
99US-0172493P.
                                                                                                                                                                                                                                                                      99US-0127409P.
99US-0134770P.
                                                                                                                                                                                                                                                                                                 99US-0125219P
                                                                         321-335; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3630 A; 744 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 vector;
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Pred. No. 8;
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                                                                                                                           useful
                                                                                                                vectors
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The present invention relates to a recombinant DNA construct (Arabidopsis thaliana) centromere. The constructs are useful producing stably inherited michrosomes which can serve as veconstruction of transgenic plant and animal cells expressing

DNA construct

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              The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (AAA01482-ADA03094), and to CC arecombinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof: The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogens or CC pathogenic trans-acting viral genes, meaning that cancer incidence is a CC direct consequence of the effects of proviral integration into host CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC cissues CA nucleic acids, proteins and antibodies are also useful as CC tissues. CA nucleic acids, proteins and antibodies are also useful as the capents and in screening and evaluating drug candidates. The present as epecifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this captain of the invention. Note: The complete sequence data for this captain did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1235; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2002; 2002WO-US041414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Nfatcl carcinoma associated gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA02717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA02717 standard; DNA; 79467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokines, antibodies, and growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant nucleic acid encoding carcinoma associated protein, ful for preparing compositions for treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAAATCCCAAACCCTAAATCTAATTCCTTAAC 7209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGCTTCTTTAAGTATTATAGTATATTTGCTCCTAAACACTAAACCCTAAACCCTACACC
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  form part of the printed cormat directly from WIPO
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Pred. No. 23;
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specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
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                                                                                                        The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                                                                                                      02-MAR-2001; 2001US-00798586
23-0CT-2001; 2001US-00004113
08-NOV-2001; 2001US-00052482
30-NOV-2001; 2001US-00997722
20-DEC-2001; 2001US-00034650
                                                                        Sequence 79467 BP;
                                                                                                                                                                                               Claim 1; SEQ ID NO 283; 2304pp; English.
                                                                                                 sarcomas.
                                                                                                                                                                                                                         cancers,
                                                                                                                                                                                                                                   New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB72455;
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                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2001; 2001WO-US051291
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                                                                                                                                                                                                                                                                                                                  (SAGR-)
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                          57;
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                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplasm; adenocarcinoma; sarcoma; gene.
TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
                                                                                                                                                                                                                         neoplasm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
                                                                                                                                                                                                                                                                                      Engelhard
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                                                                       18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
                                                                                                                                                                                                                         adenocarcinoma, or sarcomas.
                                    19.5%;
56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.5%;
                                                                                                                                                                                                                                                                                        띥
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                       0,
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                                   Score 30.6;
Pred. No. 25;
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Pred. No. 25;
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                        Mismatches
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                                                Length
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                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to novel recombinant nucleic acids for use in diagnosis and treatment of cancer, especially carcinomas, as well as the use of compositions in screening methods. The compositions of the invention may have cytostatic activity whilst the disclosed sequences may be useful for gene therapy. The carcinoma associated nucleic acids and proteins are useful for diagnosing and treating carcinomas, for example lymphoma, breast cancer, prostate cancer or leukaemia, or for screening drug candidates or bloactive agents capable of binding to, or modulating the activity of, a carcinoma associated protein. The present sequence is the genomic DNA sequence of the mouse Nfatcl gene which is a carcinoma associated gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy;
lymphoma; breast cancer; prostate cancer; leukaemia; ds; mouse; murine;
Nfatc1.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New carcinoma associated nucleic acids and proteins, useful for screening drug candidates, or for diagnosing and treating carcinomas, e.g. lymphoma, breast cancer, prostate cancer or leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 223; 793pp; English.
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                                                                                                                           TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
CACACACACACACACACACACACACACACACAGOTTGTGGCTC 53879
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Search completed: September 15, Job time : 77.0101 secs

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1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2-6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2-6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2-6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2-6/ptodata/2/pubpna/US08 NEW PUB.seq:*

7: /cgn2-6/ptodata/2/pubpna/US08 NEW PUB.seq:*

8: /cgn2-6/ptodata/2/pubpna/US08 NEW PUB.seq:*
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10230.248 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
'cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.eeq:*
'cgn2_6/ptodata/2/pubpna/US11 NEW PUB.seq:*
'cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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gn2_6/ptodata/2/pubpna/USO9E PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9 NEW PUB.seq:*
gn2_6/ptodata/2/pubpna/USO9 NEW PUB.seq:*
gn2_6/ptodata/2/pubpna/USI0A PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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20.5	31.0	100.0	100.0	
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19	222	20	20	B .
US-10-674-124A-9081	US-10-713-381-3 US-10-713-381-5	US-10-713-361-2	US-10-713-381-9	DB ID
Sequence 6, Appli Sequence 9081, Ap	Sequence 5, Appli Sequence 5, Appli	NF	Sequence 9, Appli	Description

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	53712,		Sequence 127180,	12	e 12718		21722,	21721,	e 21722,	e 21721	e 85365,	22244	222444	equence 2	22244	786	1,	۲	Sequence	Sequence 11, Appl	Sequence 2154, Ap	Sequence 179264,	e 17926	254612	e 254612,	e 57018,	_	Sequence 170626,	e 17	4,	11		equence 2	equence 244811	14	eductice 201/4'

ALIGNMENTS

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US-10-713-381-9

Sequence 9, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 579R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 255
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-9

Query Match
Best Local Similarity 100.0%; Score 157; DB 20; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.7e-43;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: APPLICANT: GARNAT, CARL W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HIPFYMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METH
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/499
PRIOR APPLICATION WALER: 08/80,499
PRIOR APPLICATION WALER: 08/80,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 1394
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; ORGANISM: Zea mays
US-10-713-381-1
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US-10-713-381-1
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Best Local Similarity
Matches 157; Conserv
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GANAAT, CARL W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: KUDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
SOFTWARE: PatentIn Ver. 2.0
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RESULT 5 US-10-713-381-5

Sequence 5, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.

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US-10-713-381-3
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SEQ ID NO 3
LENGTH: 158
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Best Local Similarity
Matches 157; Conserv
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LENGTH: 1394
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10713381 Publication No. US20040221331A1
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1275
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121
                 120 GCAACTTCCATGCAAACACGCACATATGTTTTCCTGAAC
                                                                                                                                                                                                                       157;
                                                                        61
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                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                        CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                            CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT 119
                                                                                                                                                                       CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGGTTCGTC-TTGTTCCATCGTC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
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GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTTGTTCCATCGTC
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ilarity 99.4%;
Conservative
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                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                   Score 146; DB 20;
Pred. No. 8.2e-40;
0; Mismatches 0;
158
                                    157
                                                                                                                                                                                                                                                         Length 158;
                                                                                                                                                                                                                       Indels
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US-10-674-124A-9081/c

Sequence 9081, Application US/10674124A

; Publication No. US20040197797A1

; GENERAL INFORMATION:
   APPLICANT: INOKO, Hidetoshi
   APPLICANT: TAMIYA, Gen
   TITLE OF INVENTION: GENETIC POLYMORPHISM MICROSATELLITE
   TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
   FILE REFERENCE: ORIN-003C1P
   CURRENT APPLICATION NUMBER: US/10/674,124A
   CURRENT FILING DATE: 2003-09-26
   PRIOR APPLICATION NUMBER: 10/257,511
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US-10-713-381-6
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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SEQ ID NO 5
LENGTH: 50
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APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W. APPLICANT: GARNAAT, CARL W.
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APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 578R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 40
TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.5%; Score 40; DB 20; 100.0%; Pred. No. 0.0011;
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GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robe
APPLICANT: Ohlsen, Kari
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PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: JP2000-112699
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: JP2002-327516
PRIOR FILING DATE: 2002-09-28
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2002-12-09
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LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
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                                        APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PRIOR PRIOR DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PPLICATION NUMBER: 60/207,727

PRIOR PPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR PRIOR DATE: 2000-09-06
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APPLICANT:
APPLICANT:
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APPLICANT:
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence: 250186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, R. Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind, Judith
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Pred. No. 1.3;
0; Mismatches
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PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 7001-02-16
PRIOR FILING DATE: 7001-02-16
PREMAINING PRIOR PRIOR PRIOR FILING PRIOR PRIOR FILING PRIOR PRIOR FILING PRIOR PR
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RESULT 10
US-10-027-632-244811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barbazik, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1496
LENGTH: 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local :
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                253 TCAGATCCACAAATCGCACCCTCCCATATCTGCTGAAC 216
                                                                                                                                                                                                                     120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                                                                                                                                                                                                                                 174
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                                                                                                                                                                                                                                                                                                                                               60 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
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Similarity 58.5%;
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Barbazuk, Brad
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57.1%;
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Pred. No. 5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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US-10-027-632-244811
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR PILING DATE: 1099-11-3

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002
                                                CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
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; SEQ ID NO 244811
; LENGTH: 559
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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Best Local Similarity
Matches 69; Conserv
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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FILING DATE:
                              APPLICATION NUMBER: US
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RESULT 12
US-10-052-482-223
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; ORGANISM: Human
US-10-027-632-244811
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SOFTWARE: PATENTIN VERBION 3.1
SEQ ID NO 223
LENGTH: 79467
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Best Local Similarity
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SOFTWARE: FRETSEQ for Windows
SEQ ID NO 244811
LENGTH: 559
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
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                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (13273)..(13370)
OTHER_INFORMATION: "n" at positions 13273
                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (5502)..(5521)
OTHER_INFORMATION: "n" at positions
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                           NAME/KEY: misc feature
LOCATION: (30751)..(30916)
OTHER INFORMATION: "n" at
                                                                                                         NAME/KEY: misc_feature
LOCATION: (20762)..(20781)
OTHER_INFORMATION: "n" at
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LOCATION: (10089)..(10620)
OTHER INFORMATION: "n" at positions 10089
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OTHER INFORMATION: "n" at positions 4099 to 4369 can be any base
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LOCATION: (4099)..(436)
NAME/KEY: misc_feature
LOCATION: (46579)..(46772)
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                                                                                                                                                               US-10-317-273-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/10317273
Publication No. US20040110158A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 11
                                                                                               Matches
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL
FILE REFERENCE: RTS-0478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/317,273
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kenneth W. Dobie APPLICANT: Tamara Balac Si
                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: 11187, 11188, 11189, 11190,
LOCATION: 11196, 11197, 11198, 11199,
LOCATION: 11204, 11205, 11206, 11207,
LOCATION: 11212, 11213, 11214, 11215,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 11154, 11155, 11156, 11157, 11158,
LOCATION: 11163, 11164, 11165, 11166, 11167,
LOCATION: 11171, 11172, 11173, 11174, 11175,
LOCATION: 11179, 11180, 11181, 11182, 11183,
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 11220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: 11121, 11122, 11123, 11124,

LOCATION: 11130, 11131, 11132, 11133,

LOCATION: 11130, 11139, 11140, 11141,

LOCATION: 11146, 11147, 11148, 11149,

COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (77382)..(77401)
OTHER INFORMATION: "n" at positions 77372 to 77401
                                                                                                                                                                             OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: "n" at positoins 46759 to 46772 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 52001
                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
 110 TCTTACTCATGCAACTTCCA 129
                                                    50 TTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.5%;
Similarity 56.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTC
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Pred. No. 31;
0; Mismatches
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                                                                                                              Score 30.4;
Pred. No. 31;
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                                                                                               Mismatches
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11200,
11208,
11216,
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11201,
11209,
11217,
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11168, 11169,
11176, 11177,
11184, 11185,
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11203,
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11178,
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20115 TCTTTCTCAGCAAACTTCTA 20134

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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
IENGTH: 30
TYPE: DNA
ORGANISM: Zea may8
                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-170626
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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US-10-027-632-170626
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Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
  Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                 NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 170626
LENGTH: 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 170626, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: POlymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 54
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                          19.1%;
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Score 30; DB 13; Length 843; Pred. No. 9.5; 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Gaps
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672
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                                                                               66 TTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACT 125
                                                                                                                           6 CATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCGTTGTTCCATCGTCCAAGCC
                                                       TTGCATGTGCTGGAGAGTGGGGGCTTCCGCTCCCTGCTCATCAACGCTGGGGAGGCCTCC 671
TGCATCCGAACACG
685
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Search completed: September 15, 2005, 20:45:58
Job time : 106.248 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: 9b
2: 9b
3: 9b
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Gapop 10.0 , Gapext 1.0
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157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
68479088
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UMMARIE	

Result	. Score	Query Match	Length	DB	ID	Description	ion
n		100.0	687	إو	CC656939	CC656939	OGWDQ20TV
	2 157	•	915	9	22422	CG224225	
		100.0	963	φ	CC656933	CC656933	
	37.	•	636	ø	CE588104	CE588104	
ი	w	24.1	643	7	C0689495	CO689495	DG11-25n6
	37.	24.1	1085	ø	AG366773	AG366773	Mus muscu
	u	21.7	700	N	BB505306	BB505306	0
	33.	21.4	1677	ø	CL026582	CL026582	CH216-23G
	32.	20.9	440	<u>, , , , , , , , , , , , , , , , , , , </u>	AI744861	AI744861	tr16b06.x
_	32.	20.8	804	7	CR575123	CR575123	_
o L	ω	20.8	1101	φ	CNS003FV	AL064657	
_	12 32.4	20.6	347	N	BE690384	BE690384	
	32.	20.6	483	<u>, , , , , , , , , , , , , , , , , , , </u>	AJ746802	AJ746802	АJ746802
c L		20.6	497	N	AW990724	AW990724	uf10b11.x
	32.	20.6	498	N	BE632212	BE632212	٠
	32.	20.6	500	N	BF225639	BF225639	uy44e02.x
_	32.	20.6	527	N	BE448824	BE448824	
_	32.	20.6	528	7	CN243061	CN243061	EST008934
_	32.	20.6	539	u	BX528623	BX528623	BX528623
A)	32.	20.6	542	۳	AA673664	AA673664	vo57h06.r
	32.	20.6	543	ผ	BE133867	BE133867	•
n N	32.	20.6	545	N	BF020472	BF020472	uw66f12.x
8.1	u	20.6	547	ហ	BX517541	BX517541	BX517541
o o		,	1			RE134144	10016613

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	7
31	31.2	31.2	31.2	31.2	31.4	31.6	31.8	31.8	31.8	32	32	32	32.2	32.4	32.4	32.4	32.4	32.4	32.4	32.4
19.7	19.9	19.9	19.9	19.9	20.0	20.1	20.3	20.3	20.3	20.4	20.4	20.4	20.5	20.6	20.6	20.6	20.6	20.6	20.6	20.0
463	689	633	493	446	522	685	1009	919	372	734	682	490	432	2454	2194	1039	914	859	742	17 G
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AQ376006	CA151882	CK001730	AQ811019	CA495416	N25701	BG265863	BG242888	BH168285	BY053139	BZ149047	CC480196	BF227024	BH752563	AK028832	BC048853	CNS055LA	BF682258	CNS004YY	BI453933	BB0045/5
AQ376006	CA151882	CK001730	AQ811019	CA495416	N25701 Y	BG265863	BG242888	BH168285	BY053139	BZ149047	CC480196	BF227024	BH752563	AK028832	BC048853	AL322183	BF682258	AL055406	BI453933	85004373
RPCI11-16	SCJFRZ201	AGENCOURT	HS_5382_A	AGENCOURT	725701 yx79e04.sl	1000039D0	602355872	VV_SBa000	BY053139	CH230-453	CH240_307	uz17e08.x	SALK_0188	Mus muscu	Mus muscu	Tetraodon	602117694	Drosophi.	603174018	88004373

ALIGNMENTS

Qy Db 4:	Query Match Best Local Matches 15	ORIGIN	FEATURES BOUICE	TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE	RESULT 1 CC656939/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS
1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	Query Match 100.0%; Score 157; DB 9; Length 687; Best Local Similarity 100.0%; Pred. No. 1.8e-39; Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Zee mays" /mol_type="genomic DNA" /mtrain="B73" /db_xref="taxon:4577" /clone="ZMMBMa0554015" /clone="ZMMBMa0554015" /note="Wector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"	TIGR TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends. Location/Qualifiers 1687	Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002) Other GSSs: OGWDQ20TM Contact. Cathy Whiteles		CC656939 687 bp DNA linear GSS 19-JUN-2003 OGWDQ20TV ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence. CC656939 CC656939.1 GI:32060231 GSS.

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RESULT 2
CG224225
LOCUS
                                                                       RESULT 3
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AUTHORS
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   ACCESSION
                                        DEFINITION
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963 bp OGWDQ20TM ZM_0.7_1.5 KB Zea mays genomic survey sequence. CC656933
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCA
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 915)
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGIAGOSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: whitelaw@tigr.org
Seq primer: TF
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CG224225
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK:, Site_1: HincII; 0.7-1.5
methylation filtered genomic_DNA library"
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/strain="B73"
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                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 636)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                  genomic survey sequence.
CE588104
                                                                                                                                                                                                                                                                                                                     CE588104 636 bp DNA linear GSS 2 tigr-gss-dog-17000366359543 Dog Library Canis familiaris
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Whitelaw,C.A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
                                                                                                                                                                                                              Canis familiaris (dog)
Canis familiaris
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Other_GSSs: OGWDQ20TV
 Contact: Kirkness EF
The Institute for Genomic
                                    14512627
                                                                  The dog genome: survey sequencing and comparative Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                    CE588104.1 GI:36904885
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Fax: 301-838-0208
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/clone="zyMBMa0554D15"
/clone_lib="zM.0.7 7.1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/strain="B73"
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100.0%; Pred. No. 2e-39;
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Schlueter, T., Hermanns, J., Weindel, M., Schuette, D.,
Henrich, J. and Loebbert, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CO688495 643 bp mRNA linear EST 26-JUL DG11-25n6 DG11-kidney Canis familiaris cDNA 3', mRNA sequence. CO689495.1 GI:50638161
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                                                                                                                                                                                                                                                                                                                           Tel: +49 6221 4038 150 Fax: +49 6221 4038 290
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Class: shotgun
                                                                                                                                                                                                                                                                                                                                                           Waldhoferstrasse 98, D-69123 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                             Contact: Thomas Schlueter LION bioscience AG
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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 TATTTTTTCCCAGTTCAAGGCATCCTTGTTTGGACCCAAGGGTATACCTCATTTTTAAAA
                     TCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACA 104
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                                                               Conservative
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                                                                                                                                                                                                                                                                                            Thomas.Schlueter@lionbioscience.com
Location/Qualifiers
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/note="Site 1: BstXI; Libraries were prepared
peripheral blood"
                                                                                                                                                                                                                                   /organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
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/mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                      /clone_lib="DG11-kidney"
/note="Organ: kidney; Vector:
                                                                                                                                                                                  /db_xref="taxon:9615"
/tissue_type="kidney"
/dev_stage="adult"
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58.4%;
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Pred. No. 0.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                69;
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R.Site 2
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus mol
/mol type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-170B12.TJ"
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BB505306.2
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Unpublished (2001)
On Jul 27, 2000 this sequence version repl
                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with numan Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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81-45-503-9216
/clone lib="RIKEN full-length enriched, 10 days lactation, adult female mammary gland" /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                   organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                     dev_stage="10 days lactation, lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                'sex="female"
                                                                                                                                                                              tissue_type="mammary gland"
                                                                                                                                                                                                                                        clone="D730002G06"
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Miyazaki,A., Nomura,K.,
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1677)

Kremitzki,C., Carter,J., McPherson,J., Warren,W.,
Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CL026582 1677 bp DNA CH216-23G24 Sp6.1 CH216 Xenopus tropicalis CH216-23G24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL026582
CL026582.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCTAGATTCCCAAAGAAGCCATTTTGCACTACAGTCAAACATACTAACACCCCTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCACATAT 146
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                                                                                                                                                                                                                                                                           quality sequence start: 125 quality sequence stop: 217. Location/Qualifiers
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cap-trapper. Second strand cDNA was prepared with primer adapter of sequence [5'
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/mal_type="genomic DNA"
/strain="Wilgerian frog"
/db_xref="taxon:8364"
                                                                        cell_line="Stock 248 F7A2,
                                                                                                     /sex="male"
                                                                                                                            clone="CH216-23G24"
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Pred. No.
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REFERENCE
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AI744861
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                                                                                                                 Query Match
Best Local S
Matches 61
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Best Local (
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106 TCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         829 TCATCAACTATTCTTACAGTTCATGTCACCTCCTCACTTTCTATATTATTCAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
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AI744861.1 GI:5113149
EST.
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tr16b06.x1_NCI_CGAP_Ov23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 440)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                               CTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 411.
Location/Qualifiers
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                                                                                                                                                                                             /clone_lib="NCI_CGAP_Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastassis positive. Life
Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                              tissue_type="tumor, 5 pooled (see description)"
Lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:2218451"
                                                                                                                                                                                                                                                                                                                                                             xref="mRNA"
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Pred. No. 12;
0; Mismatches
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Pred. No. 14;
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                                                                                                                                               Length 440;
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Clone I
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IMAGE:2218451 3',
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CR575123
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Best Local
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                                                                                                                                                                                                                                                                                               540
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                                                                                                                                               fly), gen
AL064657
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   Genoscope
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134 AACACGCACATATGTTTCC 152
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CR575123
5', mRNA
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                        CNSUU3FV 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08003 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: THdA024m23.plkbSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 804)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N.
Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
Contact: Croning MDR
                                                                                                                                                              AL064657.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Famphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinxton, Cambridgeshire,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGAATTATGAAAAGGCCATCTCCCATAGACTCCATTTTATGCAAGTAATTTTACATTTT 539
                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAGTATTTTTTTTCC
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                                                                                                                                                                                                          genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="XGC-tailbud-head"
/clone lib="XGC-tailbud-head"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tailbud
head. EcoRI NotI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NotI at the 3' end."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Xenopus tropicalis"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="tailbud head (stage 28-
/lab_host="Escherichia coli DH10B."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="THdA024m23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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Pred. No. 20;
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is cDNA
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THdA024m23
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REFERENCE
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TITLE
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SOURCE
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BE690384
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937 WDNBKKKBCCBMAAMARBCCRKDKKKTTYWKKTKBCYYCCYKKARGRSYKSCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          997
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                                                                                                                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 347)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE690384.1 GI:10078008
EST.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE690384 347 bp mRNA linear EST 11-SEP-2000 uw66f12.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3466991 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f:
                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE690384
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                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
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                                                                                                                                                                                              primer: -40RP from Gibco
                                                                                                                                        quality sequence stop: 270.
Location/Qualifiers
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/mol_type="genomic DNA"
/db xref="taxon:722"
/cb ref="taxon:722"
/clone="BACR08003"
/clone="BERCI-98"
/clone lib="RPCI-98"
/note="end : TET3"
/sex="female (lactating)"
                                           /mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                             organism="Mus musculus"
                         clone="IMAGE:3466991"
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Pred. No. 22;
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; Murinae; Mus
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Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Royal School for Veterinary Studies

Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM

Sequencing was performed by ARK genomics. This clone is available from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark-genomics.org or contact info@arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ746802

AJ746802 forward - stimulated minus unstimulated macrophage Sus scrofa cDNA clone F_C0001825c_D07, mRNA sequence.

AJ746802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 483)

Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, and Dixon, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development of a porcine cDNA microarray Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa
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EST.
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ACTACATECTTETTCAACCETTCETCTTETTCCATCCTAAGCCTTGCCTATTCTGAAC 80
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                                             Conservative
                                                                                                                                                          /organism="Sus scrofa"
/mol type="maRNA"
/db xref="taxon:9823"
/clone="F_C0001825c_D07"
/tissue_type="marcophage"
/colne_11bp="forward - stir
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/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was constructed by Bento Soares and M. Fatima Bonaldo.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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RESULT 15
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Best Local S
Matches 66
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
BE632212 498 bp mRNA uullf01.x1 Soares mammary gland NMLMG Mus IMAGE:3371641 3', mRNA sequence. BE632212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 497)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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uf10b11.x1 Soares_mammary_gland_
IMAGE:1510941 3', mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  TTCTTTTTCTCACCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTTGGCCTTTAAGTT 431
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                                                                                                                                                  GT 369
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
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Pred. No. 20;
0; Mismatches
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Search completed: September 16, 2005, Job time: 490.661 secs
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1. (bases 1 to 498)
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                                                                                   GT 370
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Soares mammary gland NMLMG"
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gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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APOUGS98 OZYZA BAC APOUGS710 OZYZA BAC APOU4118 OZYZA BAC APOU4786 OZYZA BAC APOU3682 OZYZA BAC APOU3682 OZYZA BAC ACU84320 OZYZA BAC AC119671 OZYZA BAC	Sequer Sequer Mus mu Mus mu Oryza	AX224397 Sequence AX224402 Sequence AX224394 Sequence AX224395 Sequence BD062177 Male tiss BD062177 Male tiss BD662176 Male mays	Description

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AP007223	OSJN00036	AC021665	AC115980	AC067922	AF242307	ATH252133	ATSUCIS	AY049275	AX506929	HIM429890	BX005189	AC101349	AC109365	AE017121	AC102160	AL626770	AC077693	AP005930	AP005916	AC090882	AC026558	AC082645	AC120884	AC120984
AP007223 Oryza sat	AL606598 Oryza sat	AC021665 Arabidops	AC115980 Mus muscu	AC067922 Homo sapi	AF242307 Euphorbia	AJ252133 Arabidops	X75365 A.thaliana	AY049275 Arabidops	AX506929 Sequence	AJ429890 Human imm	BX005189 Mouse DNA	AC101349 Mus muscu	AC109365 Oryza sat	AE017121 Oryza sat	AC102160 Mus muscu	AL626770 Mouse DNA	AC077693 Oryza sat	AP005930 Oryza sat	AP005916 Oryza sat	AC090882 Oryza sat	AC026558 Homo sapi	AC082645 Oryza sat	AC120884 Oryza sat	AC120984 Oryza sat

ALIGNMENTS

RESULT 2 AX224402 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	B &	Query Match Best Local : Matches 3	REFERENCE AUTHORS TITLE JOURNAL FEATURES BOURCE ORIGIN	KEYWORDS SOURCE ORGANISM	RESULT 1 AX224397 LOCUS DEFINITION ACCESSION VERSION
AX224402 AX224402 Sequence 9 from Patent WO0160997. AX224402 AX224402.1 GI:15554644 Zea mays Zea mays	1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30	100.0%; Score 30; DB 6; Length 30; Similarity 100.0%; Pred. No. 0.03; Onservative 0; Mismatches 0; Indels	Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 4 2-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers 130 /organism="Zea mays" /mol type="unassigned DNA" /db_xref="taxon:4577"	Zea mays Zea mays Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade. Pariocidese. Magnoliophyta; Liliopsida; Poales;	AX224397 30 bp DNA linear PAT Sequence 4 from Patent WO0160997. AX224397 AX224397.1 GI:15554639
NT 10-8EP-2001		0; Gaps 0;	and Kendall,T.L. of using same	fracheophyta; seae; PACCAD	AT 10-SEP-2001

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REFERENCE
AUTHORS
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AX224394
                                                                                                                                                                   Sequence 2 from Patent WO0160997. AX224395
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                                                              Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L. Male tissue-preferred regulatory region and method of using same Patent: WO 0160997-A 1 23-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Location/Qualifiers
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 Male tissue-preferred repatent: WO 0160997-A 2
                                                                                                           Zea mays
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                                Albertsen, M.C.,
                                                                                                                             Zea mays
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HI-BRED INTERNATIONAL, INC. (US
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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from Patent W00160997.
                                                                                                                                                            GI:15554637
                                                                                                                                                                                                                                                                                                                                                100.0%; Score 30; DB 6;
100.0%; Pred. No. 0.03;
tive 0; Mismatches 0
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                               Fox, T.W., Garnaat, C.W.,
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 regulatory region 23-AUG-2001;
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                 Huffman, G. and method
                                                                            Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACCAD
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              and Kendall,T.L.
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LOCUS
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BD062176
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KEYWORDS
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ACCESSION
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PF 19-JUN-1998 JP 1:
PR 23-JUN-1997 US
PI MARC C ALBERTSEN
PI TIMMY L KENDALL
PC C12N15/82,C12N15/
C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Sit
CC Topology: Linear
FH Key
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                               Male tissue-preferred regulatory BD062177
                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Male tissue-preferred regulatory region and method of using same Patent: JP 2001520523-A 1 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC

EN JP 2001520523-A/1

PD 30-OCT-2001

PF 19-JUN-1998 JP 1999504910

PF 19-JUN-1998 UP 199504910

PF 23-JUN-1997 US 08/680499

PR 23-JUN-19
                                                                                                   BD062177.1 GI:22607782 JP 2001520523-A/2.
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JP 2001520523-A/1.
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Location/Qualifiers
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
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/mol_type="unassigned
/db_xref="taxon:4577"
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Pred. No. 0.03;
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Pred. No. 0.03;
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Craniata; Vertebrata; E
Catarrhini; Hominidae;
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and method
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of using
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                          Euteleostomi;
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                                                                                                                                                                                                      27-AUG-2002
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Best Local Similarity
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                                                                                                                                   gene
                                                              SdS
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PD 30-OCT-2001
PD 30-OCT-2001
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN, PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC C C A01H5/00
CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1179
                                                                                                                                                                                                                                 Direct Submission
Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoidaae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF360356
Zea maye male fertility
AF360356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
                                                                                                                                                                                                                                                                                                            2 (bases 1 to 3343)
Fox, T.W., Trimnell, M.R.
                                                                                                                                                                                                                                                                                                                                         Unpublished
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ilarity 100.0%;
Conservative 0,
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19-JUN-1998 JP 1999504910
23-JUN-1997 US 08/880499
MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFMAN,
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join(1392. 1768,1898. 2182,2280.
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/codon_start=1
/product="male fertility protein"
/protein_id="AAK52489.1"
                                                                                                                                                                             /organism="Zea mays"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                       Trimnell, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                        join(<1392. .1768,1898. .2182,2280.
/gene="M845"
                                                                                                                                                /db_xref="taxon:4577"
/chromosome="9L"
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                                                                                                                     gene="M845"
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Pred. No. 0.03;
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RESULT 9
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Sequence
AX523502
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AX224396
                                                                                                                                                                                                                                                                                                                                          1 CATGCTTGTTCAACCGTTCGTCTTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                         26;
                Diadexus,
                                                               Macina, R.A.,
Compositions
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 3 23-AUG-2001, PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                               Patent: WO 02064788-A 90 22-AUG-2002;
                                                  proteins
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DGRVVRMMGEEAGWEIFAVMNPDWSEEVCANGVNSTTRKQHEKEEFCGRFLGLRFHGE
TGELYVADAYYGLMVVGQSGGYASSVAREADGDPIRPANDLDVHRNGSVFFTDTSMRY
SRKDHLNILLEGEGTGRLLRYDFETSGVHVVLKGLVFFNGVQISEDHQFLLFSETTNC
RIMRYWLEGERAGEVEVFANLFGFPDNVRSNGRGQFWVAIDCCRTPAQEVFAKKPWLR
TLYFKFPLSLKVLTWKAARRWHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK
Location/Qualifiers
                                                                                                                                                                                                                           90 from Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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                                                               Recipon, H., and methods
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89.7%;
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Patent WO0160997.
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Pred. No. 11;
0; Mismatches
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Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Northu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vansiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Ninger, S., Sainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdirim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 187192)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Cooke,P., Corum,B., Cooke,P., Corum,B., Corum,B.,
Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B., Cooke,P., Corum,B.,
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 17, clone RP23-461H1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Local Similarity
AC151282 188427 bp DNA 1:
Mus musculus chromosome 17 clone RP23-461H1,
PROGRESS ***, 12 unordered pieces.
AC151282
AC151282 GI:51511039
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                                                                                                                                                                                                                                ATGCTTGTACAACAGTTGATCTTGTTCC 52854
                                                                                                                                                                                                                                                                            ATGCTTGTTCAACCGTTCGTCTTGTTCC 29
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Center clone name: 461_H_1
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="17"
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/clone_lib="RPCI-23 Female Mouse BAC"
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9: gap of 100 bp
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0: gap of 100 bp
5: contig of 7235 bp in length
5: gap of 100 bp
5: contig of 4760 bp in length
5: gap of 100 bp
5: gap of 100 bp
6: gap of 100 bp
7: contig of 34527 bp in length
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s: gap of 100 bp
l: contig of 10055 bp in length
l: gap of 100 bp
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l: contig of 2588 bp in length
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QUENCING IN
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                                      misc_feature
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                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of read
Assembly program: Phrap; version 0.990319
Consensus quality: 182668 bases at least Q40
Consensus quality: 183763 bases at least Q30
Consensus quality: 184341 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson,R.K.
Direct Submission
Submitted (24-AUG-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 188427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: M_BA0461H01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Mus musculus clone
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    /note="assembly_name:Contig11" 1230. .2832
                                                                                organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="17"
                                                                                                                                                                                   Location
                                                               'clone="RP23-461H1"
                                                                                                                                                                  . .188427
                                                                                                                                                                                                2932 gap of unknown length
4658: contig of 1726 bp in length
4758: gap of unknown length
6427: contig of 1669 bp in length
6427: gap of unknown length
6527: gap of unknown length
11224: gap of unknown length
11224: gap of unknown length
1127: contig of 9953 bp in length
12177: contig of 10042 bp in length
1319: contig of 10042 bp in length
3139: contig of 10042 bp in length
3149: gap of unknown length
54758: contig of 23339 bp in length
54858: gap of unknown length
95904: contig of 39382 bp in length
95904: contig of 39382 bp in length
135186: contig of 39382 bp in length
135286: gap of unknown length
135286: gap of unknown length
18683: gap of unknown length
18683: gap of unknown length
186783: gap of unknown length
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E unknown
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 129778)
Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N.,
Gansberger, K., Brenner, M., Burgess, S., Hance, M., Shvartsbeyn, M.,
Tsitrin, T., Riggs, F., Hsiao, J., Zismann, V., Blunt, S., Pai, G.,
VanAken, S.E., Utterback, T.R., Feldblyum, T.V., Quackenbush, J.,
Salzberg, S.L., White, O. and Fraser, C.M.
Cyza sativa chromosome 3 BAC OSJNBb0093E13 genomic sequence
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                                                                            Direct Submission
Submitted (14-JTL-2001) The Institute f
Medical Center Dr. Rockville, MD 20850,
5 (bases 1 to 129778)
                                                                                                                                                                               Direct Submission
Submitted (11-JUL-2001) The I.
Medical Center Dr. Rockville,
4 (bases 1 to 129778)
                                                                                                                                                                                                                                                                                  Submitted (31-MAR-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA 3 (bases 1 to 129778)
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                Direct Submission
Submitted (18-JUL-2001) The Institute for Genomic Research,
                                                             Buell,R.
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  Medical Center Dr,
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186784. .188427
/note="assembly_name:Contig6"
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4759. .6427
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21278. .31319
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2933. .4658
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85.7%;
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Rockville, MD 20850,
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Pred. No. 1.4e+02;
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USA,
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                                                                                                                        Genomic Research,
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rbuell@tigr.org
                                                                                                   rbuell@tigr.
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PLN 09-AUG-2001

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-AUG-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Jul 11, 2001 this sequence version replaced gi:14042999. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSJNBb0024J04
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ICEENPODEIFDDEEEIDCEEDLDDDDDDCCSSLDDDNIECFDAEDIICLETRTWKSST
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/rpt_family="(GAA)n"
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LLLTLRCSTQPKRTRRTLPEVSPAIAGGEHENAEISDVAERNNDHVDSNIAAAEDTTF
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                       note="predicted by fgenesh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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join (<4620. 4718,4866. .>5435)
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join (4620. .4718,4866. .5435)
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   'gene="OSJNBb0093E13.5"
                                                                                                               gene="OSJNBb0093E13.5"
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chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _family="Gaijin_Os2 MITE element from gb:D10985 Rice
ne cbp3 gene for carboxypeptidase III (1125 to 1251)
                                                                                                                                                                                               family="(CGG)n"
                                                                                                                                                                                                                                                               family="(CGG)n"
                                                                                                                                                                                                                                       .4835)
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DFFYGDTLYDYETESSCDEECEHVCVCGGRCMELIDGEEFYQLITGDEFDGTQLGEEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Rice retrotransposon Tos7 DNA for reverse
transcriptase, partial cds gi|1621482|dbj|D85871.1|D85871"
complement(16049, .16146)
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12209. .12383
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codon_start=1
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/gene="OSJNBb0093E13.7"
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/codon_start=1
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AP006548
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                                                                                                                                                                                                                                                                                                                                         Pelotas, Centro de Genomica e Fitomelhoramento, Department Fitotecnia, Campus Universitario do Capao do Leao, Pelotas, Pelotas, Rio Grande do Sul 9610900, Brasil (E-mail:acostol@terra.com.br, URL:http://www.ufpel.tche.br/faem/fitotecnia/fitomelhoramento/, Tel:55-53-275-7263, Fax:55-53-275-9031)
Genes were predicted from the integrated results of the following: (http://ccR-081.mit.edu/GENSCAN.html), FGENESH (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://bioinformatics.iastate.edu/GeneMark) splicePredictor (http://bioinformatics.iastate.edu/GeneMark) splicePredictor (http://bioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iastate.edu/GeneMark) splicePredictor (http://chioinformatics.iast
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Oryza sativa nipponbare genomic DNA, chromosome 9, PAC
classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering
                                                                                                                   (ftp://ncbi.nlm.nih.gov/blast/db) and the EST sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is
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2 (bases 1 to 140729)
Oliveira,A.C., Mattos,L.T., Carvalho,F.F.,
Malone,G. and Dellagostin,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridilplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/note="predicted by fgenesh"
<21519. .>21947
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VGVDVSASNTAAAAFLPDTLALQDGVVSLAVFYLLFGVVYLLLRICALN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="OSJNBb0093E13.8"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.7%;
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family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="(GGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimano, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                 NonRedundant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The orientation of the sequence is from SP6 to T7 of the PAC clone This sequence of P0705E11 clone has an overlap with OSJNBb0069D16 clone(DDBJ: AP005882)at 5' end and an overlap with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSJNBa0038K02(DDBJ: AP005862) at 3' end
                                                                                                        /translation="MEVKVLSSRLVRPSYPASAAAPEEEFVPSSMFDKVTYDMQMAII YAFRPPGPSVADIEKGLAAVLGVYRLFAGQVVRGGGGELRGVVLNDHGARLVEACVDG SLADIAPAKPSPVVLKLHPSLEGEIEEVVQVQLTRFACGSLAVGFTANHAVADGHATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (7148. .9310)
/gene="p0705E11.2"
complement (7148. .9310)
                           GDVGGDHKQQHGHGGEEASHGIVIHKAHFTKDFIARLRAAASEGRGRPFSRFETILAH
VWRTMTRARGLGNPLQSSTIRISVDGRQRLSAPAGYFGNLVLWAFPRATVGDLLGRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTIRLSVDGRHRLGAPAEYFGNLVLWAFPRATVGDLLTRPLKHAAQVIHDEVARVDG
AYFRSFLDFALSGAGGDKEGLAPSAVLKDVLCPNAEVDSWLTFPFYELDFGTGSPTYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mevkvlssklvkpaynggvaaapdveyiplsipdkvtykmgmai
ryafpppapsynaiekglaavlagyrafagglgespdgeavvlddrgarlveaavda
dludmapakpppellkelpdlgelgevllglytrfrggslavgftsnyvvadghafs
nflvamgrafrglpmgappvhhhaalfkprpsbhvehdhrnreyylpaagddshghgd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="P0705E11.2"
/note="probably inactive due to 5' exon missing in CDS
pseudogene, GAG-POL precursor of gypsy-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P0705E11.1"
/note="probably inactive due to 3' exon missing in CDS probably inactive due to 5' exon missing in CDS probably inactive due to 5' exon missing in CDS pseudogene, orf3 of gypsy-type retrotransposon RIRE2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0705E11.1"
3382. 4071
KHAAQVIHDAVARADAAYFRSFVDFASSGAVEGEGLAPTAVLKDVLCPDLEVDSWLTF
                                                                                     DFLVAWGRAARGLAVAATAAAPPHHHPGMFRPRDPPLVEFEHRGVEYYRPPPPAAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPSYFPTEGMLFLVPSYLGDGSVDAFVPVFNHNLEAFKECCYSME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAADNI VIHKAHFTKDF IAGLRAAASEGRGRPFSRFETI LAHLWRTMTRARGLSPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (13300.
                                                                                                                                                                                              /product="putative anthranilate N-benzoyltransferase"
/protein_id="BAC79155.1"
/db_xref="GI:32490472"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative anthranilate N-benzoyltransferase"
/protein_id="BAC79154.1"
/db_xref="GI:32490471"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3382. .4071
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                                                                                                                                                                                                                                                                                                                        gene="P0705E11.4"
                                                                                                                                                                                                                                                                                                                                                                                                              'gene="P0705E11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0705E11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0705E11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0705E11.3"
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                                                                                                                                                                                                                                                                                                codon start=1
                                                                                                                                                                                                                                                                                                                                                                             note="start and end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="start and end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0705E11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="5'LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pseudo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="3/LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="P0705E11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza sativa
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                   point
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                                                                                                                                                                                                                                                                                                                                                                                   are
                                                                                                                                                                                                                                                                                                                                                                                   not
                                                                                                                                                                                                                                                                                                                                                                                identified"
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gene

mRNA gene

CDS

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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEGNOGHVEROVEGNOEEASGGQFSVGGRAAKKLEGETEN ITTEVEEDRE
SAPAEAAKNYRHSGWVFDNVFVSTVVWRRTRARGGHESVFDSEKEMLWTTWLETF
TLPTGTEDKVCKWTLKKOMADOFQSFKGDLYQKYLLKGGTFNPEDTFP FALRDHWDEFVAY
KTGEQGKAMMERNKENAAKKKYHHLGSGGYSVAMFKWEGMEASLIERGLEPATAWWP
ERSKFWYYAHGGTLNPADGSLVFGYQLGEAARRLTDAVBASGQGTFREDREDELTLA
LQTFEHFGRTGKGVLPWKLIGFKEDIHTYRSRWRSKRUTEAKIADLEFRVSSYELINMQ
EZVARKVDERMAAHRSHDPQPTLPPAMVSPSGNRSSCASTGQVGSGSGMDAMQTQDEST
CPVDDLTQRFPCELHLPFKNLSIKVASGMAIPTDESGTYLCRPIPAGSGKSVEVELVEG
AYEDLELDYFGGDGETHLRDTCHAIILMRRRYILFFRQAASRAPSFPALPSPAPDEPAPAPSFPQDPA
PSPPHAPPAPSFPQAPASTPQDDAFTPRPAFTFPPQAFLFAFSKSKRAPPAPFPAPAPHTR
AFKKAKVDAAKNNDPGYDCTQBELDAYVASEVKROPEKERPEKKLPIDFSVRNFFRGM
SASVKEAIKLSDYERTLKKASGKSKPVPQLGEQPMYRITGVAPIEKAEVKYMY
ELGKPLVKPELLQSLPFQMYKFHQLTYMEMSATGREMIGARIRDTDFLQGDDILMINFR
GIYELYQLDALDVCINSCWILMEIQRARRRRYEDTGFIDMKVNVVAMLDQYPQETEDN
LVHLLKAQHYKTFILLPYNTSFHWVLLLIDLEACTVNVVDSMDKKESTFDKVFELIDR
AWYRFRHLVRGKWRARKFKFCAKQKGGTNLCGYYVCEYCHCLADQIITTRBELDF
IRMRDNLTTHKEFIAAVQEQLMGFINEEILDERCTWOYDSMDKKESTFDKVFELIDR
AWRRFRHLTRGKBERFAKFFCAKQKGGTNLCGYYVCEYCHCLADQIITTRBELDF
IRMRDNLTTHKEFIAAVQEQLMGFINEEILDFKGEFYYDGNTIHRSLASELAASTTTS
                                                                                       /product="putative serine/threonine-protein kinase ctrl"
/protein_id="BAC79157.1"
/db_xref="GI:32490474"
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/tb_xref="GI:32490474"
/translation="MAVEEAAESCGSHAAASAAGRRGGGGGGGGATSSSSSASAGAA
AAAARKQQQQRHKLEVYTEVLRRLHDSGVPEARREGFDDELWNFRNELPARYAMDV
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LNRQQSIHPPAAFGSSTMLEALALEASKSGGDHDSTSDNVNVRPMHEITFSTIDKPK
LLSELTSILGELGINIQEAHAFSTNDGVSLDVFVVVGMHDEETEDLIESVRKEIGKID
ETGGWSTTHSWSSPVENNQIGENSAADHVEIPRDGASEWEIDVKLLKFGNKVAASGSYG
DLYRGTYCSQDVAIKVLKPERINADMQREFAQEVYIMRKVRHKNVVQFIGACTKPPNL
CIVTEYMSGGSVYDYLHKHKGVFKLPALLGVVMDVSKGMSYLHQNNIIHRDLKTANLL
MDENGTVKVADFGVARVKAQSGVMTAETGTYRWMAPEVIEHKFYDHKADVFSFGILMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0705E11.7"
join(<57646. .57935,58078. .58192,59352. .59443,59596. .59709,
59896. .59950,60105. .60215,60993. .61036,61119. .61294,
51380. .61487,62089. .62162,62257. .62432,62926. .63021,
63291. .63371,63470. .63523,64003. .64137,64210. .>64290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="start and end point are not identified"
join(57646. 57935,58078. 58192,59352. 59443,59596. 59709,
join(67646. 57935,58078. 58192,59352. 59443,59596. 61294,
59896. 59950,60105. 660215,60983. 661036,61119. 61294,
61380. 61487,62089. 62162,62257. 62432,62926. 63021,
63291. 63371,63470. 63523,64003. 64137,64210. 64290)
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/gene="P0705E11.6"
join(<49006. .50427,50502. .51258,51322. .51598,51708. .51881,
51978. .52088,52173. .52245,52340. .52438,52518. .>52703)
/gene="P0705E11.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42989. .45252
/genee"P0705E11.5"
42989. .45252
/gene="P0705E11.5"
/note="Antirrhinum majus shows structural homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /notee-"start and end point are not identified"
join(49006. .50427,50502. .51258,51322. .51598,51708. .51881,
51978. .52088,52173. .52245,52340. .52438,52518. .52703)
/gene="P0705E11.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probably inactive due to probably inactive due to probably inactive due to probably inactive due to pseudogene, transposable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maize transposon En/Spm and
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IE"
                                                                                                                                                                                                                                                                                                                                                       /codon_start=1/product="puta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="reverse transcriptase - like protein"
/protein_id="BAC79156.1"
/db_xref="GI:32490473"
                                                                                                                                                                                                                                                                                                                                                                                                                           note="contains EST(s): AU101437(E31530), AU101438(E31530)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="P0705E11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="P0705E11.7"
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mRNA gene

CDS

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Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL Submitted (05-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469]

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence as the sequence will be replaced to by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced to by the finished sequence as soon as it is available and the accession number will be preserved.
19380 CATGTTTAACCGTTCGTCTTATTCCA 19405
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group) chromosome 9 clone P0646B07,
*** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in Database (2002)
2 (bases 1 to 153675)
Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
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                                                                                                                                                                                                                                                                /organism="Oryza sativa (
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="9"
/clone="P0646B07"
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ILETLQRIAEEVGDEHDGKHKEKILGGLFSALRGRGH"
65979. _84215
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/gene="P0705E11.8"
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                                                                                                                                           Score 21.2; DB 2
Pred. No. 2.2e+02
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Pred. No. 2.2e+02;
0; Mismatches 3;
                                                                                                                  Mismatches
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                                    gene
                                                                                                                                                                                                                                                            Bource
                                                                                                                                                                                                                                                                                                                                                           On Jan 21, 200 /41; Fax: 01-29-39-79-80
On Jan 21, 200 /41; Fax: 01-29-39-79-80
Genes were predicted from the integrated results of the following:
GENSCAN (http://CGR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.html
(http://opal.biology.gatech.edu/GeneMark.html), RiceHMM
(http://www.sigr.org/tcb/glimmerm/glmr form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHMM/
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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BAC clone:OJ1148_D05.
AP004118
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                                                                                                                                                                                                                                                                                      http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
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2 (bases 1 to 155146)
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                                                                                           /organisme"Oryza sativa (
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="2"
/gene="0J1148_D05.1"
                                    /clone="0J1148_D05"
5441. .9517
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AIGKLFHSGLAHKAINAMELMNEALKEIQTWFYNDFPPHEKEKLYKFATPSTIK FTKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSRRWRWLGRNGRRGMNEERTRARR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="0J1148_D05.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="0J1148_D05.2"
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7646. .7703,8300. .8317,8422. .8544,8646. .8802,8884.
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.15178,17827. .17877,17931. .18029
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Search completed: September 16, Job time: 102.667 secs
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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                Conservative
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/note="hypothetical NorFeating NorFeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JO668. .30991

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this category is not included in IRGSP standard"
30668. .30991
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this category is not included in IRGSP standard"
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factor"
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88.5%;
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Pred. No. 2.2e+02;
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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12227.321 Million cell updates/sec
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ABQ81845	ACD26214	AAF29956	AAQ47668	ADJ40977	ADA72530	ADA71736	ADA71994	ADA72061	ADJ40785	ACA44013	ABZ13819	ABQ75351	AAH76334	AAH76333	AAH76332	AAX07409	AAX07408	AAH76340	AAH76335	ID
Abq81845 Bifidobac	Acd26214 cDNA enco	Aaf29956 Rat brain	Aaq47668 Sequence	Adj40977 Plant cDN	Ada72530 Rice gene	Ada71736 Rice gene	Ada71994 Rice gene	Ada72061 Rice gene	Adj40785 Plant cDN	Aca44013 Prokaryot	Abz13819 Arabidops	Abq75351 Human lun	Aah76334 Z. mayв М	Aah76333 Z. mays M	Aah76332 Z. mays M	Aax07409 Zea mays	Aax07408 Zea mays	Aah76340 Z. mays M	Aah76335 Z. mays M	Description

The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the M945 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

represents a DNA

fragment

-181 bases upstream

The am of

of.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

WPI; 2001-514772/56.

Claim 5; Page 47; 50pp; English.

45 18.8	C 44 18.8	43 18.8	c 42 18.8	C 41 18.8	40 18.8	18.8	38 18.8	37 18.8	36 18.8	35 18.8	34 18.8	18.8	32 18.8	31 18.8	c 30 18.8	19	19	c 27 19	19	19	c 24 19	19	c 22 19	
62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	63.3 1	63.3	63.3	63.3	63.3	63.3	63.3	63.3	
9541	7812	3339	2920	2247	2000	1908	1902	1902	1899	1083	1083	883	883	883	883	198522	5671	5671	5671	5671	1821	1388	1324	
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AAV52265	AAZ61238	ACF79841	ADM02356	ADS57809	ADJ41535	ADJ63835	ACA49918	AAS55583	ABX06821	ACA34769	AAS53644	ADI41918	ADE37244	ADD30938	ABK65288	ACN44010	ADB32792	AAS39832	ABA20915	AAK90190	ADE93879	AAC44356	ADA71777	
Aav52265 Streptoco	Aaz61238 DNA encod	Acf79841 Mouse ani	Adm02356 Human cDN	Ads57809 Bacterial	Adj41535 Plant cDN	Adj63835 Plant lip	Aca49918 Prokaryot	Aas55583 Streptoco	Abx06821 S. pneumo	Aca34769 Prokaryot	Aas53644 Helicobac	Adi41918 Plant tra	Ade37244 Plant yie	Add30938 Plant	Abk65288 Arabidops	Acn44010 Human gen	Adb32792 Human nov		Aba20915 Human ner	Aak90190 Human dig	Ade93879 Ixodes sc	Aac44356 Arabidops	Ada71777 Rice gene	

ALIGNMENTS

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RESULT 1
AAH76335
ID AAH7
XX AAH77
XX AAH7
XX AAH7
XX AAH7
XX XX Z9-C
DT 29-C
XX Zea
XX AH7
XX Zea
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    mays Ms45 male tissue-preferred regulatory region fragment.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garnaat CW,
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RESULT 2
AAH76340
ID AAH7
XX AAH7
XX AAH7
XX AAH7
XX M945
XX M945
XX M945
XX M945
XX M920
XX Zea
XX W020
XX Zea
XX W020
XX Jea
XX M921
XX M91
XX MPI

RESULT 3
AAX07408
ID AAX0
XX
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                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 30
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment
                       AAX07408 standard; DNA; 1394 BP
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 8; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514772/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mays Ms45 promoter fragment
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                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                 255 BP; 59
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                 A; 86 C;
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                                                                                                                                                                                                                                                                                                                                                 39 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      Score 30;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huffman
                                                                                                                                                   89
                                                                                                                                                                                                                                                                        0.0051;
                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                Length 255;
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                                                                                                                                                                                                                                              Gaps
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Best Local S
Matches 30
                                                                                                                                M845;
plant
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.
 23-JUN-1997;
                         19-JUN-1998;
                                                   30-DEC-1998.
                                                                            WO9859061-A1
                                                                                                       Zea mays
                                                                                                                                                                     Zea mays Ms45
                                                                                                                                                                                                08-JUN-1999
                                                                                                                                                                                                                          AAX07409;
                                                                                                                                                                                                                                                    AAX07409 standard; DNA; 1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                    1179
                                                                                                                                male; tissue-preferred; regulatory region; plant cells; tissue; differentiated; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                                  1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                   CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
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                                                                                                                                                                                               (first entry)
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                                                                                                                                                                     male tissue-preferred regulatory region.
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 97US-00880499
                         98WO-US012895
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100.0%; P
ative 0;
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Pred. No. 0.0063;
Mismatches C
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RESULT 5
AAH76332
ID AAH7
XX AAH7
XX AAH7
XX AAH7
XX AAH7
XX M845
KW M945
KW M945
KW M920
XX Zea
XX Zea
XX IS-1
PP 13-1
XX HIS-1
XX A M9
PT e88
PT A M
PT e88
PT e8
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Best Local S
Matches 30
                                                                                                                                                                                                              A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene
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                                                                                                                                                            Claim 4; Page
                                                                                                                                                                                                                                                                                                                                                                             Albertsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200160997-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea maye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M845; male tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-FEB-2000; 2000US-00504487
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30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                          46; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory region; transcription; male fertility
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Pred. No.
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RESULT 6
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Matches 30
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Matches
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                                                                                                                       The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediatring male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene exagences male fertility of the plant and (I) controls expression of the present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                   Sequence 1394
                                                                                                                                                                                                                                                       Claim 4; Page 47; 50pp;
                                                                                                                                                                                                                                                                                             A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for
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ilarity 100.0%;
Conservative (
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ilarity 100.0%;
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Pred. No. 0.0
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Pred. No. 0.0
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ABQ75351/c
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Human;
KW Human;
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Best Local S
Matches 26
                                                      Human; lung; lung specific nucleic acid; LSNA; lung LSP; cytostatic; gene therapy; vaccine; metastasis; squamous cell carcinoma; gene; ss.
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  WO200264788-A2
                            Homo sapiens
                                                                                                          Human lung specific nucleic acid sequence SEQ ID NO:90
                                                                                                                                                                  ABQ75351;
                                                                                                                                                                                           ABQ75351 standard; cDNA; 1304
                                                                                                                                                                                                                                                                                                                                                                       Sequence 158 BP; 41
                                                                                                                                       05-NOV-2002
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    mays Ms45 male tissue-preferred regulatory region fragment.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hybrid seed;
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                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                     (first entry)
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89.7%;
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Pred. No. 1.5;
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      46 T; 0 U; 0
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                                                                                                                                                                                                                                                                                                                                            5; Length 158;
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                                                                 specific protein;
lung cancer;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The present invention describes an isolated lung specific nucleic acid CC (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid CC sequences comprising 117 - 733 amino acids, given in ABB52873 to ABB52965; CC (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), CC given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b); CC or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific CC protein (LSP) sequences have cytostatic activity and can be used in gene CC monitoring the presence and metastases of lung cancer in a patient. An CC antibody that specifically binds to an LSP can be used for determining CC with lung cancer, particularly by inducing an immune response against the CC with lung cancer, particularly by inducing an immune response against the CC ung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs CC imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-CC cancerous disease states in lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
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treating
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                                                                                                                                                              24-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana stress regulated gene SEQ ID NO 1624.
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(SCRI ) SCRIPPS RES INST.
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25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recipon H,
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                                                   2000US-0227866P
2001US-0264647P
2001US-0300111P
                                                                                                                                                                2001WO-US026685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.3%;
                                                                                                                                                                                                                                                                                                                                                                                  plant; gene; stress; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen
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Query Match
Best Local Simi
Matches 24;
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Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1542 BP; 345 A; 382 C; 370 G; 445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACA44013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACA44013 standard; DNA; 2397 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prokaryotic essential gene #25670.
                                                                                                                                                                                                                                                                 (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           design;
                                                                                                                                   2003-029926/02.
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                                                                                                           ABU40143
                                                                                                                                                                                                                                                                 ELITRA PHARM
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                                                                                                                                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGATTGTTCAACCAATCGTCGGTTTCCA 266
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Carr G
                                                                                                                                                                                                                                                                 INC.
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                                                                                                                                                                                   ខ្លឹក្ខ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Pred. No. 8
                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
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                                                                                                                                                                              Ohlsen
Forsyth
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                                                                                                                                                                                      Zyskind JW;
Xu HH;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (4) an antibody capable of specifically binding cantisense expression is inhibited by the cantisense concleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular confideration; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) compound that inhibits cellular proliferation of an expansism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits ground that the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an expansism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an expression of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the confoliteration of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational conformated for proliferation to isolate candidate molecules for rational conformation or proliferation in cells other than S. aureus, S. typhimurium, compound that of the target of prokaryotic essential genes. Note: The sequence is one of the target conformation of the printed specification, but was obtained in cells correctly from WIPO at the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                           Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance;
    26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
                                                                                                                                                                                                                                                                                                                                                                                                            Plant cDNA #1785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ40785 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                      26-SEP-2002;
                                                                                                                                                             US2004016025-A1
                                                                                                                                                                                                         Eukaryota.
                                                                                                                                                                                                                                                   antifungal.
                                                                                                                                                                                                                                                                         plant nutrition; apical dominance; dwarfism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ40785;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516
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                                                                      2002US-00260238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA; 2000
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88.0%;
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RESULT 12
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cor constitutive transcription of an operatively linked nucleic acid
segment. The invention also relates to a method for augmenting a plant
cell in the seed, leaf, stem, panicle, pollen, root or is constitutive
caltered in the seed, leaf, stem, panicle, pollen, root or is constitutive
in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
serghum, rice or wheat. The polynucleotides and the polypeptides they
cencode are useful for manipulating crop plants to alter or improve
phenotypic characteristics, to produce large quantities of oil or
incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
have a high nutritional value with reduced apical dominance or dwarfism,
early flowering or altered metabolic pathways. This sequence represents a
plant nucleic acid of the invention. Note: The sequence data for this
patent did not form part of the printed specification but was obtained in
celectronic format directly from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 23
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                              WO2003000898-A1
                                                                                    Oryza sativa
                                                                                                                                                                                                                              Rice gene, SEQ ID 5386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                        Plant; bacterial infection;
                                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                      ADA72061 standard; DNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to plant nucleotide sequences that direct seed., leaf- and/or stem-, panicle-, root- or pollen-specific or -preferentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Budworth P, Moughamer T, Briggs SP, Goff SA, Katagiri F, Kreps J, Prova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BUDW/)
(MOUG/)
(BRIG/)
(COOP/)
(COOP/)
(GLAZ/)
(GOFF/)
(KATA/)
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GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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PROVART N.
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COOPER B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1785; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                    (first entry)
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82.1%;
                                                                                                                                                                     fungal infection; viral infection;
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Pred. No. 1.2e+02;
0; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ricke D,
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e D, Zhu T;
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RESULT 13
ADA71994/c
ID ADA719
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Best Local S
Matches 22
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Katagiri
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                                                                                                                                                                                                                      Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.
                                                                                                                                                                                                                                                     Rice gene, SEQ ID 5319
                                                                                                                                                                                                                                                                                                     ADA71994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2000 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                    WPI; 2003-175290/17.
                                                                                                    22-JUN-2001; 2001WO-IB001105
                                                                                                                          22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                        WO2003000898-A1
                                                                                                                                                                                               Oryza sativa
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                                         Chen W, Cc
F, Quan S,
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F, Quan S,
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                                                                                                                                                                                                                                                                            (first entry)
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                                           Cooper
S, Tao
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S, Tao Y,
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Pred. No. 1.
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                                          Glazebrook J, G
Whitham S, Xie
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ie Z, Zhu
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ie Z, Zhu
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Identifying at least one gene involved in plant resistance or response

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RESULT 14
ADA71736 E
ID ADA71736 E
XX
AC ADA71736;
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DT 20-NOV-200
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Plant; bac
XX
Plant; bac
XX
POTZA BAT!
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POTZA BAT!
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Best Local !
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                The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
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  corresponding for conferring
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F, Qu
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S, Tao
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84.6%;
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                                                                                                                                                                                                                                                                             one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
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RESULT 15
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XW Plant;
XW Plant;
XX Oryza
PN WO2003
XX Identi
PT Chang
PI Katagi
XX WPI; 2
XX Identi
PT Pathog
PT Bacter
PT Gene e
XX Claim
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Best Local S
Matches 22
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Best Local
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Katagiri
                                                                                                                                                                         involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying at least pathogenic infection bacterial, fungal or
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; Patent No. 6037523
; GENERAL INFORMATION:
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Fox, Tim W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COMMUTER PROCES:
COMMUTE
                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vers

LURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,499

FILING DATE: CONCURRENTLY HEREWITH

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Sweeney, Patricia A.

REGISTRATION NUMBER: 32,733

REFERENCE/DOCKET NUMBER: 32,733

REFERENCE/DOCKET NUMBER: 0578

TELEPHONE: (515) 248-4800

TELEPAX: (515) 248-4800

TELEFPAX: (515) 248-4844

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1394 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-880-499-1
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11327, Appli 16445, A 9, Appli 9, Appli 12574, A 12574, A 17490, A 17614, A 13614, A 17504, A 169, App 178197, 820, App 11034, A 11034, Ap 11034, Ap

Title: Perfect score:

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1179

CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30

CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208

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                                                                                                                                                                                                                             RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-880-499-2
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                                                                                                                                             Sequence 15, Application US/07937609
Patent No. 5319073
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                         APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
ADDRESSE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REGISTRATION NUMBER: 0578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. STREET: Boox 1000
CITY: Johnston
                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                  1179 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
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30; Conserv
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Alexandria
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               3: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1394 base pairs
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; llarity 100.0%; Pred. No. Conservative 0; Mismatch
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Mismatches 0
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RESULT 4
US-08-029-170-15
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Best Local Simi
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FILING DATE: 1920902

CLASSIFICATION: 436

PRIOR APPLICATION UNMBER: US 07/831,248

APPLICATION UNMBER: US 07/861,769

FILING DATE: 07-FEB-1992

PRIOR APPLICATION UNMBER: US 07/861,769

FILING DATE: 01-APR-1992

PRIOR APPLICATION UNMBER: US 07/928,033

APPLICATION UNMBER: US 07/928,033

APPLICATION INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VA
COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: WANK,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                 APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDN/
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                          COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: rat brain CCKB receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703, 503, 4109
                                                                                                                                                CITY: Alexandria
                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2243 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
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 PatentIn Release #1.0, Version #1.25
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79.3%;
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Pred. No. 49
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CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/937,609

FILING DATE: 02-SEP-1992

CURRENT APPLICATION DATA:

PPLICATION NUMBER:

19930310

US/08/029,170

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992

PRIOR APPLICATION DATA:

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Best Local Sim:
Matches 23;
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                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6706493
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 |
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                  COUNTRY: USA
ZIP: 22313-0299
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPORTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
CLASSIFICATION:
PRIOR APPLICATION DATA:
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LOCATION:
                                     FILING DATE:
                                                                                                                                                                                                                                  CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: rat brain CCKB receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/861,769 FILING DATE: 01-APR-1992
                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09443745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.7%; Score 19.4;
79.3%; Pred. No. 49;
                                                    US/09/443,745
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; ORGANISM: Human US-09-949-016-16262
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US-09-949-016-16262
                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 16262
LENGTH: 45571
Query Match 63.3%;
Best Local Similarity 81.5%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16262, Application US/09949016 Patent No. 6812339
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Best Local (
                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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TELEFAX: 899149
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: rat brain CCKB receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 07-FEE
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23; Conservative
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nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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01-APR-1992
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 Score 19; DB 4; Le
Pred. No. 1.3e+02;
0; Mismatches 5;
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Pred. No. 49;
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                                Length 45571;
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Gaps
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38119

TGCTTGTTCAACCGTTCGTCTTGTTCC TGTTTGTTCATTCGTTCTTCTTCC 38145

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US-09-368-590-1/c

RESULT 7

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                                                                                              ; ORGANISM: Human US-09-949-016-1438
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Query Match
Best Local Similarity 76.7
Conservative
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMERER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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SEQ ID NO 1
LENGTH: 7812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Solimena, Michele
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
FILE REFERENCE: 101918-200 (CCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1999-08-07
UNMBER: OF SEQ ID NOS: 8
                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                       TYPE: DNA
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COCATION: (1021)...(1023)
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LOCATION: (100)...(102)
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LOCATION: (2266)...(2268)
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NAME/KEY: CDS
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                                                                                                                                                        ENGTH: 8756
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                                 62.7%;
76.7%;
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76.7%;
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Pred. No. 1.1e+02;
0; Mismatches 7;
                0
                                 Score 18.8; DB 4; Length 8756; Pred. No. 1.2e+02;
                Mismatches
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OF DETECTION AND USES THEREOF
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                Indels
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RESULT 10
US-09-949-016-13180/c
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Sequence 13180, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 132, Application US/08961527 Patent No. 6420135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VETB
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/96
EILING DATE:
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charles TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELECOPTION (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.7%;
Local Similarity 76.7%;
hes 23; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9541 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                         CAGGCTTGTCCAAACGTTCCATTTTTTCCA 8078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.8; DB 3;
Pred. No. 1.2e+02;
0; Mismatches 7;
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US-09-270-767-13492/c

; Sequence 13492, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 13492

; LENGTH: 1120

; TYPE: DNA

ORGANISM: Drosophila melanogaster

US-09-270-767-13492
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US-09-270-767-29480
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US-09-270-767-29480/c
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                                                             Query Match
Best Local S
Matches 21
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29480
LENGTH: 549
TYPE: DNA
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SOFTWARE: FastSEQ for
SEQ ID NO 13180
LENGTH: 112874
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Best Local S
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LOCATION: (1)...(112874)
OTHER INFORMATION: n = A,T,C
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                                                                              Similarity
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TGCTTGTTGAAGAGTTCTTCTTGTT
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                               TGCTTGTTCAACCGTTCGTCTTGTT 27
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ilarity 84.0%;
Conservative
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for Windows Version
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76.7%;
                                                                            62.0%;
84.0%;
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Pred. No. 1.9e+02;
0; Mismatches 7;
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Pred. No. 84;
0; Mismatches
                                                             ..
                                                                            Score 18.6;
Pred. No. 96;
                                                             Mismatches
199
                                                                                            DB
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                                                                                          Length 1120;
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ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: repeat_region
LOCATION: (1)..(2710)
OTHER INFORMATION: charlie3
NAME/KEY: misc feature
OTHER INFORMATION: n is a, c, g or t
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: PROCECTPIC sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution
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US-09-573-080A-7/c
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LENGTH: 1260
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09573080A Patent No. 6828097 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3293, Application US/09248796A
PATENT NO. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AN
TITLE OF INVENTION: FOR DIAGNOSTICS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 7
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SINGLE COPY GENOMIC F
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
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                                                                                                                                                     ISSUE: 4
PAGES: 286-291
DATE: 1992-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JOAN, KNOLL APPLICANT: ROGAN, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.132
                                                                                          ORGANISM: Candida albicans
                                                                                                                                                                                                                VOLUME: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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78.6%;
                60.7%;
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                Score 18.2; DB 4;
Pred. No. 1.7e+02;
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Pred. No. 1.2e+02;
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                                                                                                                                   for repetitive elements (repbase)
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                                      4
                                  Length 2710;
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Oy 3 TCCTTGTTCAACCAGTTCGTCTT 27

Db 1209 TGCTGTTCACCAGTTCGTCTKGTT 1185

RESULT 15
US-09-949-016-200252/c
Sequence 200253, Application US/09949016
PRICE NO. 6812398
FREENAL INFORMATION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
THEREFERENCE: CLOO1307
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION UMBER: C0/031/498
PRIOR FILLING DATE: 2000-04-14
PRIOR APPLICATION UMBER: C0/237,768
PRIOR
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Minimum DB
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No.
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

22: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

23: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

24: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

25: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*

26: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*
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US-10-713-381-9
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US-10-713-381-3
US-10-713-381-3
US-10-001-857-90
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10230.248 Million cell updates/sec
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Sequence 4, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 90, Appl
Sequence 6815, Ap
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ALIGNMENTS

RESULT 1 US-10-713-381-4

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Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 30
                                              Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                  TYPE: DNA
  1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                 Conservative
                                          100.0%; Score 30; DB 20;
100.0%; Pred. No. 0.0065;
htive 0; Mismatches 0;
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RESULT 4
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; ORGANISM: Zea mays
US-10-713-381-1
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 1394
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Best Local S
Matches 30
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KUDFMAN, TIMMY L.
APPLICANT: KUDRALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 255
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Best Local
                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, GARY
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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ORGANISM: Zea mays
                                                        1179 CATGCTTCTTCAACCGTTCGTCTTGTTCCA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 68
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                                                                                                                                                Score 30; DB 20
Pred. No. 0.011;
                                                                                                                                Mismatches
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PRIOR APPLICATION NUMBER: 08/880,499
PRIOR TILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 158
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-3
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US-10-713-381-3
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                                                                           Query Match
Best Local Similarity
Matches 26; Conserv
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1394
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10713381 Publication No. US20040221331A1
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: KUEMAL, GARY
APPLICANT: KUEMALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEC IN NO. 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10713381 Publication No. US20040221331A1
                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 24
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25
                           1 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
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ilarity 100.0%;
Conservative (
                                                                               Conservative
                                                                                              89.7%;
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                                                                           Score 24.2; DE Pred. No. 2.2; 0; Mismatches
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Pred. No. 0.011;
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                                                                                                                       DB 20;
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                                                                                                                   Length 158;
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US-10-001-857-90/c
, Sequence 90, Application US/10001857
, Publication No. US20020183500A1
, GENERAL INFORMATION:

APPLICANT: Macina,

RESULT 6

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Sequence 17676, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT

FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILLING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17676
                                                                                                                                                                                                                                                                                                                                                      밁
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; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-719-993-6815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-719-993-6815/c
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; ORGANISM: Homo sapien
US-10-001-857-90
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Best Local Similarity 82.8%;
Matches 24; Conservative
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SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 6815
LENGTH: 1980090
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILLING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-11-24
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TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: ALZHEIMER'S DISEASE,
FILE REFERENCE: CL001496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 208
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25; Conserv
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Liu, Chenghua
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Pred. No. 1.7e+02;
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METHODS OF
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DETECTION AND
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1624
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
ITITLE OF INVENTION: STRESS-REGULATED GENES OF PLJ
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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US-09-938-842A-1624
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                                                                                                                                                                                                                                                                                   Sequence 1624, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 80.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana
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Pred. No. 1.7e
0; Mismatches
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Pred. No. 1.2e+02;
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1.7e+02;
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NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1624
LENGTH: 1542
                                                                 Query Match
Best Local (
                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 31883
LENGTH: 2397
TYPE: DNA
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Best Local &
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                 Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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ORGANISM: Arabidopsis thaliana
                                                                                                                                  ORGANISM: Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/253,625
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                  1 CATGCTTGTTCAACCGTTCGTCTTG
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                                                 Similarity 88.0
22; Conservative
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Forsyth, R.
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הירח, Robert
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                                                                 Score 20.2;
Pred. No. 1.
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Pred. No. 1.
                                                                 .6e+02
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CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1785
LENGTH: 2000
TYPE: DNA
OFFICIAL SECTION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1785
LENGTH: 2000
                                   ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94716C.1
US-10-437-963-96639
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US-10-437-963-96639/c
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                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                               TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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Query Match
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Publication No. US20040016025A1
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                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
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Katagiri, Fumiyaki
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Briggs, Steven P.
Cooper, Bret
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Ricke, Darrell
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65.3%;
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Pred. No. 1.
Score 19.6;
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DB 19;
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Length 640;
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CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR PELLING DATE: 2001-09-26
PRIOR PELLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1977
SEQ ID NO 1977
SEQ ID NO 1977
SEQ ID NO 1977
ORGANISM: OTYZA BALÍVA
US-10-260-238-1977
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US-10-260-238-1977/c
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; OTHER INFORMATION: Clone ID: MRT4577_103225C.1
US-10-425-115-3534
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US-10-425-115-3534/c
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322) B
FULE REFERENCE: 38-21 (5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 3534
LENGTH: 901
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1977, Application US/10260238 Publication No. US20040016025A1 GENERAL INFORMATION:
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Best Local S
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Zea maye
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108 22; Conservative
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Pred. No. 2.5e+02;
0; Mismatches 4;
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Result
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ALIGNMENTS

SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CC656939/c LOCUS á 밁 ORIGIN COMMENT FEATURES REFERENCE DEFINITION Query Match Best Local Similarity Matches 30; Conserv AUTHORS source 397 1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 687) 1 (bases 1 to 687) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics CC656939 OGWDQ20TV ZM 0.7_1.5_KB genomic survey sequence. CC656939 Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends. Unpublished (2002) Other_GSSs: OGWDQ20TM 9712 Medical Center Drive, Contact: Cathy Whitelaw CC656939.1 GI:32060231 **Zea mays** CATGCTTGTTCAACCGTTCGTCTTGTTCCA 368 Conservative /clone="ZMMBMa0554D15" /clone | 1b="ZM_0.7_1.5_KB" /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 methylation filtered genomic DNA library" /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" Location/Qualifiers 100.0%; 0, Score 30; DB Pred. No. 0.0 0; Mismatches Zea 687 bp Rockville, mays genomic clone ZMMBMa0554D15, 0.02; B DNA 9; MD 20850, USP 0 Length 687; Indels linear GSS 19-JUN-2003 0; ፎ Gaps 0

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RESULT 3
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                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 963)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robins,D. and Lakey,N. Consortium for Malze Genomics

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1 (bases 1 to 915)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Unpublished (2002)
Other GSSs: OGIAGOSTH
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CG224225 CG224225.1 GI:34124113
GSS.
Zea mays
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Other_GSSs: OGWDQ20TV
Contact: Cathy Whitelaw
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Class: sheared
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Fax: 301-838-0208
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1 (bases 1 to 308)

Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                  190 Frelinghuysen Road, Piscataway, NJ
Tel: 732 445 3801
Fax: 732 445 5735
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Tel: 301-838-5843
Fax: 301-838-0208
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Location/Qualifiers
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Class: BAC ends
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The Plant Genome Initiative at Rutgers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
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Class: sheared
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                                                                                                                                                                                                                                                                                                                                   Email: bharti@waksman.rutgers.edu
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QHJ7N19.yg.ab1 (
clone QHJ7N19, r
BU035739
BU030489 626 bp QHJ15I20.yg.abl QH_EFGHJ sunflower clone QHJ15I20, mRNA sequence.
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1 (bases 1 to 534)

1 (Kozik, A., Michelmore, R.W., Knapp, S., Matylenko, M., Rieseberg, L. Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lei, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                           2 ATGCTTGTTCAACCGTTCGTCTTGTT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OH_CA_Contig3046, see http://cgpdb.ucdavis.edu/
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1-(530)-752-9659
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/clone lib="QH EFGHJ sunflower RHA280"
/note="Vector: pBRcDNASfiAB; The library was constructed from 1 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
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TAG_LIB-QH_EFGHJ sunflower RHA280
TAG_SEQ-CGAATGCGGG"
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/mol_type="mRNA"
/cultivar="RHA280"
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                                                                                                                                                                                                                                                                            Score 21.2; DB 5;
Pred. No. 1.5e+02;
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RHA280 Helianthus
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
                                                                                                                                                                                                CN137013 792 bp mRNA linear EST 01-APR-20 OX1_54 E01.gl A002 Oxidatively-stressed leaves and roots Sorghum bicolor CDNA Clone OX1_54_E01_A002 5', mRNA sequence.
CN137013
                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower BSTs from the Compositae Genome Project
                                                                                                  Sorghum bicolor
                                                                                                                                                                           CN137013.1 GI:45970259
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                          Sorghum bicolor (sorghum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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(bases 1 to 792)
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/note="Vector: pBRcDNASfiAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUE=flowers environmental stress
TAG_LIB=OH_EFGHJ sunflower RHA280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="RHA280"
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2H_CA_Contig3046, see http://cgpdb.ucdavis.edu/
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Pred. No. 1.5e+02;
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154 bp mRNA linear EST 19-FEB-1998 oa99e03.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320412 3' similar to SW:COPE_BOVIN Q28104 COATOMER EPSILON SUBUNIT;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 154)
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An EST database from Sorghum: oxidatively stressed leaves and roots
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                              Unpublished (1997)
                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Contact: Cordonnier-Pratt_MM
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA811551.1 GI:2881162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.7%;
llarity 88.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="OX1_54_B01_A002"
/clone="OX1_54_B01_A002"
/lab host="DH10B-TI phage-resistant E. coli"
/clone lib="Oxidatively-stressed leaves and roots"
/clone lib="Oxidatively-stressed leaves and roots"
/note="Organ: Leaf and Root; Vector: pME185-F13; Site_1:
/note="Organ: Leaf and Root; Vector: pME185-F13; Site_1:
/note="Organ: Leaf and Root; Vector: pME185-F13; Site_1:
/note="Organ: Leaf and Root; Vector: pME185-F13
/roote most and Root; Vector: pME185-F13
/roote most and Root; Vector: pME185-F13
/roote most and leaves
/roote misted with hydrogen peroxide to 0.003 and leaves
/roote misted with 10 uM methyl viologen. Leaves and roots
/roote misted with 10 uM methyl viologen. Leaves and roots
/roote misted with 10 uM methyl viologen. Leaves and roots
/roote misted with 10 uM methyl viologen. Leaves and roots
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/roote misted with 10 uM methyl viologen. Leaves and roots
/roote misted with 10 uM methyl viologen. Leaves and roots
/roote misted with 10 uM methyl viologen.
/roote misted with 10 uM meth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sug5 (CTTCTGCTCTAAAAGCTGCG).
cation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _type="mRNA"
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Pred. No. 1.6e+02;
0; Mismatches 3;
                                                                                                                                                        Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 792;
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REFERENCE
AUTHORS
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VERSION
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DEFINITION
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CR192459/c
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Matches
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Best Local Similarity
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                                                                                                                                      JOURNAL
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                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciu 1 (bases 1 to 351)
Adams,D.J., Biggs,P.J., Cox,A.V., Jonkers,J., Smith,J., Plumb,R.W., Rogers,J. and Bradley,A.
                                                                                                                                                                                                                                                                                                                                                                                         CR192459 351 bp DNA Reverse strand read from insert in 5'HPR' chromosome engineering clone MHPN146a06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                      Submitted (20-FEB-2004) Sanger Centre, Hinxton,
                                                                                                                                                                                                                                                                                                                                                      CR192459
CR192459.1 GI:49971308
                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence; MICER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality Insert Length: 1232 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Con., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                    CB10 1SA,
                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Senome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCTTGTTAAACCCATCGTCCTGTTCCA 15
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    Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N
and Eco RI sites of the modified p77T3 vector. Library
went through one round of normalization, and was

/mol_type="genomic DNA
/db_xref="taxon:10090"
/clone="MHPN146a06"
                                                                                             UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by Bento Soares and M. Fatima Bonaldo."
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/db_xref="taxon:9606"
/clone="IMAGE:1320412"
/tissue_type="germinal_center_B_cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/mol_type="mRNA"
                                                       organism="Mus musculus"
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82.8%;
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Pred. No. 1.5e+02;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                             DNA linear GSS 06-JUL-20 in 5'HPRT insertion targeting and
                                                                                                                                                                                             Davies,R.M.,
Taylor,R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 154;
                                                                                                                                                                                                                                                                                                                                                                                             genomic
                                                                                                                                                                                             Nishijima, I.,
                                                                                                                                                                                                                  van der Weyden,
                                                                                                                                                                                                                                                                                                                                                                                             Burvey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      David Allman,
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                                                                                                                                                                                                                                                      Murinae; Mus.
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SOURCE
ORGANISM
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AUTHORS
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CR233964/c
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AUTHORS
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CR064270/c
                                                                                                                                                                                                                                                                VERSION
KEYWORDS
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                                                                             FEATURES
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                                                                                                                    Eukaryota; Metazoa; Chordata; Crani; Mammalia; Eutheria; Rodentia; Sciurr 1 (bases 1 to 599)
Adams,D.J., Biggs,P.J., Cox,A.V., D. Jonkers,J., Smith,J., Plumb,R.W., T. Rogers,J. and Bradley,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                          309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                             Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN144h08, genomic survey sequence. CR233964 CR233964.1 GI:50012813 GSS; genome survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR064270. GI:49797742
CR064270.1 GI:49797742
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 571)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y Rogers,J. and Bradley,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR064270 571 bp DNA linear GSS 05-JUL-200 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN190119, genomic survey sequence.
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                                                                                       Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                              GSS; genome survey sequence; Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:10000"
/clone="WHPN190119"
/clone_11b="MHPN"
 /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN144h08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .571
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                               organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%;
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82.8%;
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Pred. No. 1.8e+02;
0; Mismatches 5;
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Pred. No. 1.7e+02
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                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                   Davies, R.M., Taylor, R.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 571;
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                                                                                                                                                   van der Weyden,L.,
Nishijima,I., Yu,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire,
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ORGANISM
                                                                                                                      REFERENCE
AUTHORS
TITLE
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CC848693/c
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AUTHORS
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KEYWORDS
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VERSION
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CR188179/c
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                                                                                            COMMENT
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                                                                                                                                                                                                                   ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310
                                                                          1 (bases 1 to 832)
Loftus,B., Shetty,J., Knudson
BAC end sequencing of Aedes a
Unpublished (2003)
Other GSSs: NDL.2114.SP6
Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                          307
                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
9712 Medical Center Drive,
Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR188179
CR188179.1 GI:49967028
                                                                                                                                                                                  Neoptera; Endopterygota;
                                                                                                                                                                                                                                                               CC848693.1 GI:33197857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                                                                                                                                                            NotreDame Liverpool-2114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="MHPN"
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82.8%;
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Pred.
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No.
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Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexar
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                      CC848693 832 bp DNA linear GSS NDL.2I14.T7 Notre Dame Liverpool Aedes aegypti genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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                                            Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN234h03"
                                                                                                                                                                                                                              Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Indopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                    Knudson, D. and
Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Rockville,
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No. 1.9e+02;
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MD 20850, USA
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Nishijima,I., Yu,Y.,
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REFERENCE
AUTHORS
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CC860012/c
LOCUS
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SOURCE
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 Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local S
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NDL.2II3.T7 Notre Dame Liverpool Aedes aegypti genomic clone
NotreDame Liverpool-2II3, genomic survey sequence
CC860012
CC860012.1 GI:33220022
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ATSCTTSTTCAACCSTTCSTCTTSTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library was provided by David Severson Seg primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                     Email: enta@tigr.org
Library was provided
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 835)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
                                                                                                                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends.
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Contact: Brendan Loftus
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aedes aegypt
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Unpublished (2003)
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                                                                                                         /clone="NotreDame Liverpool-2113"
/clone lib="Notre Dame Liverpool"
/clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and
                                                                                                                                                                                                    /organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="NotreDame Liverpool-2114"
/clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
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82.8%;
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 Score 21; DB Pred. No. 1.9e 0; Mismatches
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Pred. No. 1.9e+02;
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VERSION
KEYWORDS
Search completed: September Job time: 93.5658 secs
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AUTHORS
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ORGANISM
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R12648
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                                                                                                                                                 Local Similarity
                                                                 313
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 1704
High quality sequence stops: 276 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1704
Std Error: 0.00
Seq primer: M13RP1
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yf57f08.rl Soares infant brain
TMAGE: 26260 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 276.
Location/Qualifiers
                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="GDB:398607"
/db_xref="taxon:9606"
/clone="IMAGE:26260"
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                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
                                                                                                                                             68.7%;
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                  2005, 08:08:43
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                                                                                                                              Score 20.6; DB 7;
Pred. No. 2.6e+02;
0; Mismatches 4;
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Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         St. Louis,
                                                                                                                                                             Length 412;
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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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14440.280 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.	Score	Query	Query Match Length	BB	ID
, р	40	100.0	40	6	AX224399
N	40	100.0	50	0	AX224398
ω	40	100.0	158	σ	AX224396
4	40		255	თ	AX224402
ហ	40	100.0	1394	σ	AX224394
თ	40	100.0	1394	o	AX224395
7	40	100.0	1394	0	BD062176
œ	40	100.0	1394	σ	BD062177
9	40	100.0	3343	8	AF360356
c 10	30.4	76.0	137327	8	AC135206
11	24		55001	9	AC084290
c 12	24	60.0	127196	10	AL807784
13	24		171940	N	AC148514
14	23.6	59.0	193735	N	AC148501
15	23	57.5	117026	9	AC008897
16	23	57.5	149232	N	AC102478
17	23	57.5	177104	N	AC125876
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22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.4	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.8	22.8	22.8	23	23	23	
55.5	55.5	55.5	55.5	55.5	55.5	55.5	55.5	55.5	56.0	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	57.0	57.0	57.0	57.5	57.5	57.5	
176084	157574	153814	152797	150489	111122	73885	71561	21700	112361	235953	196990	186457	175110	170973	161817	160246	130893	95896	235928	175781	164944	319056	242109	234163	
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AC113354	AL592293	AP003180	AC016856	AC069491	ATF11C1	AC025307	AL928982 6	BX322645	HS39B17	AC130117	AC134013	AC129669	AP002428	AP000923	AC132119	AC009221	AC149638	AL356384	AE003736	AC008091	AC008195	AC016640	AC147523	AC115318	
AC113354 H	AL592293 H	AP003180 H	AC016856 H	AC069491 H	AL132976 A	AC025307 H	Continuation (7 of	BX322645 H	AL023656 H	AC130117 R	AC134013 R	AC129669 R	AP002428 H	AP000923 H	AC132119 Mus	AC009221 H	AC149638 M	AL356384 H	AE003736 D	AC008091 D	AC008195 D	AC016640 H	AC147523 O	AC115318 R	
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ALIGNMENTS

DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 2 AX224398 REFERENCE AUTHORS TITLE RESULT 1 AX224399 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM FOCUS ORIGIN FEATURES Query Match Best Local : Matches JOURNAL source y Match 100.0%; Score 40; DB 6;] Local Similarity 100.0%; Pred. No. 4.2e-05; hes 40; Conservative 0; Mismatches 0; Zea mays Zea mays Zea mays Zea mays AX224398 50 bp Sequence 5 from Patent WO0160997 AX224398 Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 6 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers AX224399 40 bp Sequence 6 from Patent WO0160997. AX224399 AX224398.1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; 2ea. AX224399.1 /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" GI:15554641 GI:15554640 DB 6; Length 40; DNA DNA Indels linear linear and Kendall, T.L. of using same PAT 10-SEP-2001 PAT 10-SEP-2001 0, Gaps 0

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Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Sequence 9 from Patent WO0160997.
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Male tissue-preferred regulatory region Patent: WO 0160997-A 9 23-AUG-2001;
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htive 0; Mismatches 0;
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Male tissue-preferred regulatory region patent: WO 0160997-A 2 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
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Sequence 2 from Patent WO0160997.
AX224395
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clade; Panicoideae; Andropogoneae; Zea.
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Pred. No. 3.4e-05;
Mismatches 0;
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a; Poales; Poaceae; PACCAD
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PRED INTERNATIONAL INC
PN JP 2001520523-A/1
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W PI TIMNY L KENDALL
PC C12N15/85, C12N15/29, C12N9/24, C12N9/22, C07K14/34, C12Q1/68, PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
CC
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                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                               Male tissue-preferred regulatory region and method of using BD062177
BD062177.1 GI:22607782
UP 2001520523-A/2.
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Male tissue-preferred regulatory region and Patent: JP 2001520523-A 2 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC PN JP 2001520523-A/2
                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Albertsen, M.C., Fox, T.W., Garnaat, C.W.,
Kendall, T.L.
                                                                                                                    1 (bases 1 to 1394)
Albertsen, M.C., Fox, T.W., Garnaat, C.W.,
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MARC C ALBERTYSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFMAN,
TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
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[larity 100.0%; Pred. No. 2.8e-05;
Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PF 19-JUN-1998 JP 1999504910
PF 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMP
PI TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC
PC C12N15/00
PC A0115/00
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
FH Key Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-MAR-2001) Trait and Technology Development, Pionee: Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 3343)
Fox,T.W., Trimnell,M.R. and Albertsen,M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning of Ms45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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19-JUN-1998 JP 1999504910
23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
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DYRPVGHELAPYGEVMGSWFRDNASKLRRGKLEFVGEVFGFESEFDLQGRGPYAGLA
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TGELYVADAYYGLMVVGQSGGVASSVAREADGDPIRFANDLDVHRNGSVFFTDTSRFHGE
STRLTVADAYYGLMTFAVDPETSGVHVVLKGLVFFNGVQISEDHQFLLFSETTNC
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RIMRYWLEGPRAGEVEVFANLPGFPDNVRSNGRGQFWVAIDCCRTPAQEVFAKRPWLR
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/cod--
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/protein_id="AAK52489_1"
/db_xref="GI:14028757"
                                                                                                                                                                                  /product="male fertility
join(1392. .1768,1898. .2
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                                                                                                                                                                                                                                                   /gene="M845"
                                                                                                                                                                                                                                                                                                       db_xref="taxon:4577"
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Pred. No.
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                                                                                                                                                                                   :y protein"
.2182,2280.
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REFERENCE
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AC135206/c
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                                          source
                                                                        Submitted (16-Apr-2003) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA On Jan 11, 2003 this sequence version replaced gi:24635891.

This sequence was finished as follows unless otherwise notes: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality -30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-33874 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69957-70761, 89336-90416, 98551-99009, 105316-105607, and 133052-133152 are covered by Monaanto only. The nucleotide sequence of this BAC clone was generated by combining Syngenta, Monaanto and Arizona Genomics Institute sequencing data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submittee And Andreas (1998) Arizona, 303 Forbes, Tucson, AZ 85721, USA S. (bases 1 to 137327) S. (bases 1 to 137327) Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T., Wing,R.A., Yu,Y., Soderlund,C., Simmons,J., Thurmond,S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-NOV-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA (Dases 1 to 137327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-OCT-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA 3 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J., Collura,K. and Thompson,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Currie,J., Collura,K. and Thompson,S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JAN-2003) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Collura, K. and Thompson, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice
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Wing, R.A., Yu, Y., Sode
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AC135206.3 GI:27596977
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LWIGTVAHNHIATIPYPLED"
               /organism="Oryza sativa (japonica cultivar-group)"
                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; 100.0%; Pred. No.
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/gene="0J1041F02.4"
                                                                                                                                                                                                                 21819. .24660
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/db_xref="taxon:39947"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                16734. .16878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="unknown protein"
/protein_id="AAP06845.1"
/db_xref="GI:29893591"
                                                                                                                                                                                                                                                                                                                    gene="0J1041F02.3"
                                                                                                                                                                                                                                                                                                                                                             note="putative transposon,
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|gene="OJ1041F02.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAP06844.1"
/db_xref="GI:29893590"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="unknown protein"
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/note="putative MITE, Gaijin/Gaigin-like"
19263. .19454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPPQQGECCRHGWLGVGEAAVGGGGEEPFYVPLRKRLSVDGKAS
TAPRICIWECGGEAGDITCDLYAAPLARSCSAKAMPPPAPLFRWMTPPPPRPQGGDGE
EARRPGEAIRGHRSYSLMLMILQLGISYSVGKSSALPFQKLDASSDPDPREKTWTRFPP
EGSKFTPPHHSVDFRWKDYCPAVFRHLRKLFGVDPAEYMLAICGNDTLRELASPGKSG
SCFFITQDDRFMIKTWKKSFWVLIRWLRSYYEHVRQYKSTLLTRFYGTHCIKQAGOP
KIHRREDLKGSSHGRTIDKTERKIDENTTLKOLLQVAFRHLGRFWYEELMKQIOMDCT
FLETQGIMDYSLLLGVHFRNDYSVSKIGISQHIAFPKSTGKRKSFEGGSSFCELCFVE
/trānslation="MATASDGSGSGEQRRILSIPKEGERIIAPTRRPDGTLRKAIRI
RAGYVPQEEYAIYGSKGAQWKKSGPDVPPGYDPALDAKPKTKAAKRNEERKEKRQQAS
TTNDXGKGKHIEDDAGETDNAKDASUSOTKOJSGIAISESLVVATSSTDATDNAKSES
SAPDIDKKIRALKKKIRLAEAQVQGDPENLKPEQLEKMKKIEGWKEELKLLENKSSPA
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3513. .3727,3812. .3934,4024. 4054,4157. .4216,5088. .5243,
5312. .5411,5484. .5699,5808. .5942,6035. .6538,6622. .6837,
7548. .7593,7679. .7815,8196. .8328,9221. .9495))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFGIIDILQDYDITKKLEHAYKSFQVNPDYISAVDPKLYSRRFQDFIRRVFIKEQ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGCKDRDLIDSRKPFIQLGINMPAQAERSSKKILDNFLLNERHLFITPPSGGSCDVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unknown protein"
join(12372. .12757,12858. .13025,13130. .13295,13716. .1
13982. .14130,14224. .14354,14459. .14558,15197. .15503)
/gene="031041802.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESDEVKTVVAKAVSHLISVYGQQMQPILSALPPAHANALASFANRR"
                                                                                                               /product="hypothetical protein"
/protein_id="AAP06846.1"
/db_xref="GI:29893592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="(japonica cultivar-group)"
complement(638. .9495)
                                                                                                                                                                                                                                                                .22206,23772. .23996,24523. .24660)
                                                                                                                                                                                                                                                                                                                                                                             CACTA, En/Spm-like"
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Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative MITE, Castaway-like" complement (59793. .62196) /gene="OJ1041F02.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein"

/complement(join(35049. .35184,35866. .36033,36922. .37205,

37280. .38523,40038. .40104.40196. .40287,404066. .40617,

37280. .38523,40038. .40104.70196. .40287,40406. .43753,

41678. .41760,42229. .42529,42907. .43088,43694. .43753,

44229. .44426,44622. .44676,45877. .45992,46149. .46313,

46447. .46620,47271. .47470,47915. .48019,48200. .48263,
                                                                                                                                                                                  /note="putative MITE, MITE-adh, type G-like'
51474. .51836
                                                                                                                                                                                                                                                                                                                                  ATDDGFVDFLQELLFSGTTTTSLGKFVSSGISCGDGSGNISHVKYPTSCISKRRERQA
RLREVLLPVVPPKLSQSLRGPAFVDYLSSMSQISQLENMQLSECKASSKQRRCRQPRH
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complement(31668. .31815)
complement(35049. .49855)
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LEHPFVNRSMRSIRSMRTSSRSNSSILVLLIMWSWPGRTIRYREAILSTAQSSTPTIA
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EGISDEGVFFAVKEVCLCDGSAAQQCTGVLBGEIALLGQFEHBIVQYYGTDKEDSK
LYIFLELVTQGSLASLYQKYBLRDTHVSAYTRQILNGLTYLHERNIVHBDIKCANILV
HANGSVKLADFGLAKEITKFNVLKSCKGTVYMMAPEVVNPKTTYGPEADIWSLGCTVL
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PVADWEAHKAGRSSFSSSASTPKPREEPPARDSPVRREVAAEEEPPSLPAPAAAPVLP
AKETPRSVAIEAPAPLLRVDPWEPARPDVRKASGEGGIKGVRPPPVVLKPPPSMVRPA
VCVVESTWDILRSFAPEEDSHAHAPASRSGGDSACQDAGEEEDDAAAVLTLEELRLGE
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27881. .27940,28051. .28126,28327. .28484,28616. .28678,
28790. .28874,29560. .30575))
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/protein_id="AAP06848.1"
/db_xref="GI:29893594"
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/translation="MGPPAAPPSPSSSSGGSSRRRRLERRNAAKHIGYDASNFCAYP
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  Score 30.4; DB 8; Length 137327; Pred. No. 0.12; 0; Mismatches 6; Indels 0;
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El (bases 1 to 55001)

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 55001)

Mingo, M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chocko, J., Chavez, D., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Dalaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Earnhart, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Johnson, R., Jolivet, S., Joudah, S., Karlsoyle, J., Kyan, U., Landry, N., Landry, 
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                                                                                                                                 Submitted (21-OCT-2000) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 55001)
                                              Worley, K.C.
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Direct Submission
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Submitted (27-MAR-2002) Human Genome Sequencing Center, Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
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STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
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complement(2156. .2209)
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                                            Conservative
                                                                                    /rpt_family="Aluy"
complement(23147.
/rpt_family="MIR"
                                                                                                                          /rpt_1
22796.
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complement(12975. .1308
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complement(7309. .7
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22682. .22789
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complement(20660. .20
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                                          Score 24; DB Pred. No. 48; O; Mismatches
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                                                                                                                                110413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep RP23-448C18 is from the RPCI-23 Mouse PAC Library—

For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bequence.
AL807784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    humquery@Banger.ac.uk Clone requests: clonerequest@Banger.ac.uk
On Nov 15, 2002 this sequence version replaced gi:24939941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-NOV-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  AC148514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL807784.11
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                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                AGGATACATAAGCCAAATCAACCTTTCTTACTAATGCCAC 110374
                                                                                                                                                              AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                             clone="RP23-448C18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                        60.0%;
75.0%;
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                                                                                                                                                                                                                               Score 24; DB 10; Length 127196;
Pred. No. 43;
0; Mismatches 10; Indels 0;
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HTG 24-MAR-2004
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some X, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross missassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coleman, H., Daki, N., Engle, J., Granité, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 24, 2004 this sequence version replaced gi:45332443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 171940)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Papio.
1 (bases 1 to 171940)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with a Phrap-derived quality score.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                  NOTE:
                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 1100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 171395 bases at least 040
Consensus quality: 171621 bases at least 030
Consensus quality: 171701 bases at least 020
Insert size: 173000; agarose-fp
Insert size: 171740; sum-of-contigs
Quality coverage: 8.33x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 171940)
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                                                                                                                           This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- Genome Center
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,S., Guan,X., Gupta,J.,
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Best Local S
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                                                                                                                                                                                                                    Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, H., Daki, N., Engle, J., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-tin, S.-O., Legaspi, R., Madden, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Park, M., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC1485013
GI:50080339
HTG: HTGS_PHASE2; HTGS_DRAFT.
Callithrix_jacchus (white-tufted-ear marmoset)
Callithrix_jacchus
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                                         Submitted (10-MAR-2004) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 193735)
                                                                                                                                                                                    NISC Comparative Sequencing Initiative Unpublished
                           Green, E.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC148501 193735 bp DNA linear HTG 09-JUL-20
Callithrix jacchus clone CH259-368E20, WORKING DRAFT SEQUENCE, 11
                                                                                                                                               Green, E.D.
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 10148: contig of 10148 bp in length 10149 10248: gap of unknown length 10249 103023: contig of 92775 bp in length 103024 103123: gap of unknown length 103124 171940: contig of 68817 bp in length 103124 171940: dentig of 68817 bp in length 103124 171940: dentig of 68817 bp in length 103124 171940: dentig of 68817 bp in length.
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                                                                                                                      Submission
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clone_end:T7
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103124. .171940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNJ
/db_xref="taxon:9555"
/clone="RP41-375M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RP41"
/note="BAC resource: http://bacpac.chori.org/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Papio anubis"
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Pred. No. 42;
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source

/mol_type="genomic DN /db_xref="taxon:9483" /clone="CH259-368E20"

organism="Callithrix jacchus"

_type="genomic DNA"

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * consists of 11 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 29310 29409: gap of unknown length

* 29310 37712: contig of 29309 bp in length

* 37813 40472: contig of 8303 bp in length

* 37813 40472: gap of unknown length

* 40473 40572: gap of unknown length

* 40473 40572: gap of unknown length

* 40473 40572: gap of unknown length

* 10472: contig of 5152 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 190717 bases at least Q40
Consensus quality: 191709 bases at least Q30
Consensus quality: 192323 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 192735; sum-of-contigs
Quality coverage: 13.33x in Q20 bases; agarose-fp
Quality coverage: 9.96x in Q20 bases; sum-of-contigs
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63313
70561
70661
                                                                 10375
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------ Project Information

Center project name: fv

Center clone name: 368E20
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                         ocation/Qualifiers
.193735
                                                                                                                                                            4: gap of unknown length
7: contig of 13083 bp in length
7: gap of unknown length
2: contig of 2085 bp in length
2: gap of unknown length
0: contig of 7248 bp in length
0: gap of unknown length
0: gap of unknown length
8: contig of 2998 bp in length
8: contig of 2998 bp in length
8: gap of unknown length
                                                          contig of 29895 bp in length
gap of unknown length
contig of 89982 bp in length
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                                                                                                                                                                 Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 117026)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                     Direct Submission
Submitted (07-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Nov 7, 2000 this sequence version replaced gi:7711370.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC008897 117026 bp DNA linear PRI 07-NOV-
Homo sapiens chromosome 5 clone CTD-2235C13, complete sequence.
AC008897 GI:11119448
HTG.
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.5.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          2 (bases 1 to 117026)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                         lomo sapiens (human)
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ilarity 76.3%;
Conservative
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clone_end:SP6
vector_side:right"
127712. 193735
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70661. 73658
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63313. .70560
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40573. .45724
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1. .29309
/note="assembly_fragment
clone_end:T7
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103754. .193735
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73759. .103653
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Pred. No. 60;
0; Mismatches
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                                                      72634 AGGAAACGGATTAACAAACTATCCACCTTTCTCAAGCAA 72672
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WI-9815 G05428
SHGC-16751 G15410
WI-7171 G06431.
                                                                      1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                                                                             Similarity
                                                                                                            57.5%;
ilarity 74.4%;
Conservative
                                                                                                                                                                                                /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                   /clone="CTD-2235C13"
                                                                                                                                                                                                                                      organism="Homo sapiens")
                                                                                                                                                                                                                                                        .117026
                                                                                                              0,
                                                                                                                           Score 23; DB 9;
Pred. No. 1.1e+02;
                                                                                                              Mismatches
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12227.321 Million cell updates/sec
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Listing first 45
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Copyright (c) 1993 - 2005 Compugen Ltd.
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21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.6	21.6	21.6	21.6	22.4	40	40	40	40	40	40	40	40	Score
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ABL03396	AAS63328	ABL32928	ABL54304	ABL32155	ABZ13750	ADS89580	ADE84196	ADB54282	ABL32304	ABZ10202	ACN45146	AAH76333	AAH76332	AAX07409	AAX07408	AAH76340	AAH76334	AAH76336	AAH76337	ID
Abl03396 Drosophil	Aas63328 Chemicall	Abl32928 Human imm	Abl54304 Chemicall	Abl32155 Human imm	Abz13750 Arabidops	Ads89580 Oligonucl	Ade84196 Human lym	Adb54282 Pretreate	Abl32304 Human imm	Abz10202 Haematopo	Acn45146 Human gen	Aah76333 Z. mays M	Aah76332 Z. mays M	Aax07409 Zea mays	Aax07408 Zea mays	Aah76340 Z. mays M	Aah76334 Z. mays M	Aah76336 Z. mays M	Aah76337 Z. mays M	Description

The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription the WS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

present sequence represents a DNA

fragment upstream

provided. The TATA box of

of.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

WPI; 2001-514772/56.

Claim 14; Page 32; 50pp; English.

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5	44	43	42	41	40	39	38	37	36	S	34	33	32	31	30	29	28	27	86	25	24	23	22	21
20.8	20.8	20.8	20.8	20.8	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
52.0	52.0	52.0	52.0	52.0	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5
110000	6620	6620	6620	891	106315	63294	63294	63294	63115	10286	10286	8404	8404	8404	8404	8404	8404	8404	8404	5507	5507	3117	2792	2000
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AAI61373_1	ABN80279	ABK28416	AAS45488	ABZ51893	ACN43966	ADM74534	ADB72677	ADA02939	ADC85419	ABK28147	AAS45308	ADS89516	ADS89242	ADE84152	ADE84076	ADB54088	ADB54216	ABL33595	AAS46500	ABZ10058	ABZ10204	ADM98942	ADM98941	ADJ41594
Continuation (2 of	Abn80279 Human che	Abk28416 DNA trans	Aas45488 Chemicall	Abz51893 Aspergill	Acn43966 Human gen	Adm74534 Murine ca	Adb72677 Mouse Tle	Ada02939 Mouse Tle	Adc85419 Mouse Tle	Abk28147 DNA trans	Aas45308 Chemicall			Ade84152 Human lym	Ade84076 Human lym	Adb54088 Pretreate	Adb54216 Pretreate	Abl33595 Human imm	Aas46500 Tumour su	Abz10058 Haematopo	Abz10204 Haematopo	Adm98942 Diterpene	Adm98941 Diterpene	Adj41594 Plant cDN

ALIGNMENTS

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RESULT 1
AAH76337
ID AAH7
13-FEB-2001; 2001WO-US004527.
                                                                                                                                                                        WO200160997-A2
                                                                                                                                                                                                 Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.

    mays Ms45 male tissue-preferred regulatory region fragment.

                                                                                                                                                                                                                                             AAH76337;
                                                                                                                                                                                                                                                          AAH76337 standard; DNA;
                                                                                                         Albertsen
                                                                                                                                                           23-AUG-2001.
                                                                                                                                                                                     Zea mays.
                                                                                                                                                                                                                                 29-OCT-2001
                                                                                                                     (PION-) PIONEER HI-BRED INT INC
                                                                                                                                 15-FEB-2000; 2000US-00504487.
                                                                                                         ă,
                                                                                                                                                                                                                                (first entry)
                                                                                                         Fox
                                                                                                       W.
                                                                                                                                                                                                                                                          40
                                                                                                         Garnaat CW,
                                                                                                                                                                                                                                                          BP.
                                                                                                         Huffman
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                                                                                                         Kendall TL;
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AAH76334
ID AAH7
                  RESULT 3
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Best Local S
Matches 40
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AAH76334 standard; DNA; 158
                                                                                                                                          The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -11 bases upstream of the TATA box of a Z. mays MS45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                       A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                     Sequence 50
                                                                                                                                                                                                                                      Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                             WPI; 2001-514772/56.
                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                                                                                       WO200160997-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mays Ms45 male tissue-preferred regulatory region fragment.
                                                                                                                                                                                                                                                                                                                                                 15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                  M845; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH76336 standard;
                                                                                                                                     nucleotide sequence
                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                            hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mays Ms45 male-tissue preferred regulatory region nucleotide sequence
                                             11
                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                            seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                           AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                               <u>გ</u>
                                                                                                                   BP; 18 A; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                              Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                              Garnaat CW,
                                                                                                                    C; 5
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BP.
                                                                                0;
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                                                                                Score 40; DB
Pred. No. 3.7
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No.
                                                                                                                   G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                               Huffman
                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                .7e-06;
;8 0;
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                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
                                                                                                                                                                                                                                                                                                              Kendall TL;
                                            50
                                                             40
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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RESULT 4
AAH76340
ID AAH7
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a male tissue-preferred regulatory region (1) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediatring male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (1) into a plant where the exogenous gene impacts male fertility of the plant and (1) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the producing hybrid seeds in the present sequence represents a DNA fragment -38 to -195 bases upstream of the present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
                                                                                                                                                                         AAH76340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for
                       Ms45; male tissue; regulatory region; transcription; male
                                                                       mays Ms45 promoter fragment.
                                                                                                                        29-OCT-2001
                                                                                                                                                                                                                       AAH76340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514772/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2000; 2000US-00504487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mays Ms45 male
hybrid seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                 L
                                                                                                                                                                                                                                                                                                                                                                            AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                     standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 BP; 41 A; 50 C;
                                                                                                                                                                                                                                                                                                                                                  AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fertility in a male plant
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative (
promoter;
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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  ds.
                                                                                                                                                                                                                          255
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 5; 1
Pred. No. 4.4e-06;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 G; 46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                              40
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                       fertility;
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WO200160997-A2 23-AUG-2001.

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RESULT 5
AAX07408
ID AAXC
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Best Local S
Matches 40
                                                                                New nucleic - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment
                                                                                                                        WPI, 1999-105628/09.
                                                                                                                                                                                                                               19-JUN-1998;
                                                                                                                                                                                                                                                                                    WO9859061-A1
                                                                                                                                                                                                                                                                                                          Zea mays.
                                                                                                                                                                                                                                                                                                                                                                          Zea mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX07408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is
                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                     23-JUN-1997;
                                                                                                                                                                                                                                                          30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 8; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514772/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                       tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
                                                                                                                                                 <u>გ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š,
                                                                                                                                                                                                                                                                                                                                     tissue-preferred;
e; differentiated;
                                                                            acid encoding a Ms45 male tissue-preferred regulatory region mediating plant fertility, especially hybrid seed production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                       22-23;
                                                                                                                                                FOX
                                                                                                                                                                                                   97US-00880499
                                                                                                                                                                                                                               98WO-US012895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 1394
                                                    39pp; English
                                                                                                                                                Garnaat CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garnaat
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P
                                                                                                                                                                                                                                                                                                                                                 regulatory region; plant cells;
                                                                                                                                                                                                                                                                                                                                     maize; hybrid seed; fertility; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 5;
Pred. No. 4.7e-0
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                                                                                                                                                Huffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
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RESULT 6
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Best Local S
Matches 40
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                                                                                                                                              The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                           Sequence 1394
                                                                                                                                       and infertile
                                                                                                                                                                                                                                                                              Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                Albertsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays Ms45 male tissue-preferred regulatory region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX07409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1998;
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1239
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                                                                                                                                                                                                                                                                                                                                                    1999-105628/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               male; tissue-preferred;
tissue; differentiated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                    40;
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                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            PIONEER HI-BRED
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AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                      AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                    Conservative
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                                                                                                         BP;
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                                                                                                                                     plants
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                                                                                                         411 A; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                                 100.0%; Score 40; DI
100.0%; Pred. No. 6.:
tive 0; Mismatches
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                                                                                                           C; 232
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulatory region; plant cells; hybrid seed; fertility; ss.
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                                                                                                           442 T; 0 U; 0 Other;
                                                               6.1e-06;
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                                                                                DB 2;
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                                                                             Length 1394;
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                                                    Indels
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RESULT 8
AAH76333
ID AAH7
XX AAH7
XX AAH7
XX 29-C
XX 29-C
XX Y 19-C
XX M845
XX M845
XX M845
XX M951
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                             comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M845; male tissue;
hybrid seed; ds.
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    mays Ms45 male tissue-preferred regulatory region encoding

                                                                                                                                                                                                                                                                                                                                                                      Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 46; 50pp; English.
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               WO200160997-A2
                                                                  Ms45; male tissue;
hybrid seed; ds.
                                                                                                                                       29-OCT-2001
                                                                                                                                                                                           AAH76333 standard; DNA; 1394 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514772/56.
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                                         Zea mays.
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                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                              AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory region; transcription; male fertility;
                                                                               regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                              6.le-06;
                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                                                          Length 1394;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising nucleotide sequences essential for initiating transcription of the M345 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1394 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exogenous gene. A method of producing hybrid seeds is also present sequence represents a nucleic acid sequence encoding tissue preferred regulatory region from Z. mays
                                                               Recombinant nucleic acid useful for diagnosis
                                                                                         WPI; 2003-328604/31.
                                                                                                                                                                        01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                        WO2003073826-A2
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                          Cytostatic; carcinoma; lymphoma; cancer; human;
                                                                                                                                                                                                                                                                                                                                   Human genomic sequence hCG1639824
                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                          ACN45146;
                                                                                                                                                                                                                                                                                                                                                                                                                   ACN45146 standard; DNA; 226215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2001; 2001WO-US004527
                                                 comprises a nucleotide sequence.
                                                                                                                                                                                                  28-FEB-2003; 2003WO-US006235
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                                                                                                                                                                                                                             12-SEP-2003
                                                                                                                                             (SAGR-) SAGRES DISCOVERY.
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                                                                                                                     JW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 5; 1
Pred. No. 6.1e-06;
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                                                                treatment
                                                                of carcinoma
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The present invention relates to novel DNA and

protein sequences which

SEQ ID NO 1948; Opp; English.

Claim 1;

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RESULT 10
ABZ10202/c
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                                                                         The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG which distinguishes between methylated and non-methylated CpG
dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used
                                                                                                                                                                                                                                                                                                                  Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
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A, Lipscher E, Maier S,
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Model F,
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Mueller V,
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R, Leu E;
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diagnosis and treatment o methylation.

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chemically associated

modified gene,
with abnormal

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immune system associated

acute myeloid

lsorders, sequences

The present invention provides a number of human immune system assoc: genes which are modified by the methylation of cytosines. The sequent can be used in the diagnosis and treatment of immune system disordern including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo: leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

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Best Local (
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy;
bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
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RESULT 12
ADB54282/c
Query Match
Best Local S
Matches 24
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Best Local S
Matches 27
                                                                                                                                                                                                                     The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent or series of reagents, where the reagent or series of discinctions within the target nucleic acid. The molecules of the dinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The NNA (peptide nucleic acid)-oligomers are useful as probes for determining are restricted.
                                                                                                                                                     determining cytosine methylation state or single nucleotide polymorphisms. The current sequence is that of the pretreated genomic region of the invention. This sequence is not shown within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cell proliferative disorder; non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB54282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis, diseases. The present
                                                                                                                                    specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-731620/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kujan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2002; 2002EP-00004551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2003; 2003WO-EP002035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003072821-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pretreated genomic DNA region 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB54282 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
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27; Conserv
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                          Similarity
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                                                                                            7110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitt A;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                          BP;
                                                                                                                                       Jud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 1758 A;
                                                                                          1818 A; 0
                                                                                                                                       is taken
                     54.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                       from
Score 21.6; D
Pred. No. 1.5e
0; Mismatches
                                                                                          C; 1721 G; 3571 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.6; D
Pred. No. 1.5e
0; Mismatches
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                                                                                                                                  Wipoweb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nimmrich I,
                     .5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5e+02
                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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    Indels
                                        Length 7110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
  Gaps
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RESULT 13
ADE84196/c
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                                                                             cc acid. The genes and/or their regulatory regions are preferably selected cf from MDR1, CSNK2B, EGR4, AR, CDR4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDCN1B, CDKN2B, CDKN2B, CC GSTP1, HIC-1, MGWT, MLH1, MOS, WYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C, CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the CC Gpd dinucleotides within one or more the sequences, or their complements, CC for determining the cytosine methylation state and or single nucleotide collections such as diffuse large B-cell lymphoma, mantle cell lymphoma, CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, CC lymphoma. They are also useful for detecting of a predisposition to, CC differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between the least one reagent or series of reagents that distinguish between the least one reagent or series of reagents that distinguish between the least one reagent or series of reagents that distinguish between the least one reagent or series of reagents that distinguish between the least one least of the least or series of the least of the least or series of the least of the least or series of the least of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; SEQ ID NO 192; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-457621/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of detecting and differentiating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2001; 2001DE-01057491
28-DEC-2001; 2001DE-01064501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003044226-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE84196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-2002; 2002WO-EP013265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lymphoid cell proliferative disorder gene derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3083
                                                               mentioned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACCTACTCCCAAACAATCCATCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caldwell C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                            genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,Β
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
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Query Match Best Local Similarity

54.0**%**; 85.7**%**;

Score 21.6; DB 10 Pred. No. 1.5e+02;

DB 10;

Length 7110;

Sequence

7110

B₽;

1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;

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RESULT 14
ADS89580/c
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                                                                                                                                              The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a trarget nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is used to the exemplification of the invention.
                                                            Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting responsiveness of a subject with breast cell proliferative disorder, useful for treating or differentiating breast cell proliferative disorders comprises analyzing methylation pattern of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002; 2002DE-01045779
07-JAN-2003; 2003DE-01000096
17-APR-2003; 2003DE-01017955
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                               genomic DNA from the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; cell proliferative disorder; breast; methylation; cytostatic;
gene therapy; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide of the invention SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADS89580 standard; DNA; 7110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-348468/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nimmrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foekens J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003; 2003WO-EP010881.
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                                                                            Similarity
AMACCTAACCCCAMACAATCCATCCTAC 3056
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                   ATACCTACTCCCAAACAATCCATCTTAC 31
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Rujan T,
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                                                             Conservative
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Schmitt
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                                                          Score 21.6; DB 13;
Pred. No. 1.5e+02;
0; Mismatches 4;
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Schmitt M,
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I, Look MP,
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Marx A;
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Search completed: September 15, 2005, 21:33:23 Job time: 20.3656 secs

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ABZI3750/c
ABZI3750/c
ABZI3750;
XX
AC ABZI3750;
XX
DT 21-JAN-2003 (first entry)
XX
Arabidopsis thaliana stress regular
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KW Arabidopsis thaliana.
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KW Arabidopsis thaliana.
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KW W0200216655-A2.
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PN W0200216655-A2.
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PPN W0200216655-A2.
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PPN W0200216655-A2.
XX
PPN 24-AUG-2001; 2001WO-US026685.
XX
PPN 22-JUN-2001; 2001US-0300111P.
XX
A (SCRI ) SCRIPPS RES INST.
PA (SYGN ) SYNGENTA PARTICIPATIONS AC
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A (SYGN ) SYNGENTA PARTICIPATIONS AC
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PR (SYGN ) SYNGENTA PARTICIPATIONS AC
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                                                                                                                                    Matches
                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                          The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thatiana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this pattent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana; plant; gene; stress; transgenic; ds
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288
                                                                                                                                    28;
                                                                                                                                                                    Similarity
                                          AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA
AGTCCACCTATTCCCCAAACAATCTCTGTGCCTCACACAA
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                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                        460 A; 231 C; 319 G;
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Pred. No. 1.
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Minimum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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Match Length DB
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10817.505 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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   aggaracctactccaaacaatccatcttactcatgcaac
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               US-08-880-499-1
US-08-880-499-2
US-09-248-796A-5546
US-09-949-016-14995
US-09-949-016-13668
US-09-949-016-11844
US-08-949-016-11842
US-09-949-016-11824
US-09-949-016-13193
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US-09-949-016-13231
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Sequence 2, Appli
Sequence 5546, Ap
Sequence 1995, A
Sequence 65770, A
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            Sequence
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  184, Appli
13668, A
11120, A
11123, A
11123, A
2016, Appli
8655, Appli
8655, Appli
8655, Appl
13221, Appl
13221, Appl
19002, A
19002, A
19002, A
19002, A
17437, Ap
17437, Ap
15779, A
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US-08-880-499-1
            Query Match 100.0%; Score 40; DB 3; Best Local Similarity 100.0%; Pred. No. 4.6e-07; Matches 40; Conservative 0; Mismatches 0;
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48.5	48.5	48.5	48.5	48.5	48.5	49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0
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Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence								
333, App	5447, Ap	202761,	74160, A	74129, A	26227, A	14141, A	17192, A	13667, A	15715, A	12659, A	16090, A	29, Appl	15506, A	1, Appli	83111, A	83110, A	1562, Ap

ALIGNMENTS

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NUMBER OF SEQUENCES.

CORRESPONDENCE ADDRESS:
ADDRESSEE:
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Patent No. 6037523
; GENERAL INFORMATION:
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TTITLE OF INFORMATION MALE TISSIE- D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AND METHOD OF USING SAME NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
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AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC

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US-09-248-796A-5546
; Sequence 5546, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: FOR DIAGNOSTICS AND THER
FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILLING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
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US-08-880-499-2
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPHONE: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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STREET: Box 100
CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1394 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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1998-02-13
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lding, 7100 N.W. 62nd Ave., P.O
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                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                         AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN AND THERAPEUTICS
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ches 0;
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Best Local Similarity
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Best Local Similarity
Thes 26; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Human US-09-949-016-14995
                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-65770/c
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                                                   PATENT NO. 6812339

PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEG ID NOS: 207012
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LENGTH: 42075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5546
LENGTH: 1071
TYPE: DNA
ORGANISM: Candida albicans
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 65770 LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                       Sequence 65770,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31591 ATTCCTACCCACAAACCATCCATCTTA 31565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATACCTACTCCCAAACAATCCATCTTA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCCCACTCTCAAACATGTCAACTTACTTATTCA 258
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85.2%;
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Pred. No. 1.2e
0; Mismatches
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Pred. No. 51;
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FILE PERFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOPTWARE: pt_FL_genes Version 2.0
SEQ ID NO 184
LENGTH: 973
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; ORGANISM: Human
US-09-949-016-65770
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Best Local (
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Best Local Similarity
                                                                                         GENERAL INFORMATION:
APPLICANT: Coupland, George M.
APPLICANT: Putterill, Joanna J.
TITLE OF INVENTION: Genetic control
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Drmānac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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NAME/KEY: CDS
LOCATION: (231)..(749)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 973
TYPE: DNA
ORGANISM: Homo sapiens
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STREET: 8th Floor, 1100 No. 60779
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                        626 GGAAATCAACTCCAAAAGAAACCCTCGAAACCATGCAA 663
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5. 6743619
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
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Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehrman, Tom
                                                      B: Nixon & Vanderhye PC
Bth Floor, 1100 No. 6077994th Glebe Road
                                                                                                                                                                                                                                                                                                                                                       Conservative
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71.1%;
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                    Score 20.4;
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                            of flowering
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                                       US-09-949-016-13668
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT ELING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13668
LENGTH: 51770
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                                                      NAME/KEY: misc_feature
LOCATION: (1)...(51770)
OTHER INFORMATION: n =
                                                                                                                   ORGANISM: Human
FEATURE:
                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: Landsber POSITION IN GENOME: MAP POSITION: ch
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,056
FILING DATE: 20-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9-
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
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LENGTH: 4201 base pair
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APPLICATION NUMBER: PCT/GB95/02561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ms Mary J Wilson REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2631 GATACCAGCTCCCACCATCAAACTTACT 2660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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51.0%;
                                                          A,T,C or
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Pred. No. 85;
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Query Match

Score 20.4;

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Length 51770;

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; LOCATION: (1).T. (84571)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-11824/c
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 17420
LENGTH: 84571
TYPE: Nor:
                                                                                                                                                PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11824
LENGTH: 126200
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local
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                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001307
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(126200)
OTHER INFORMATION: n = A,T,C or
                                                                                                       ORGANISM: Human
                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24559 GGAAATCAACTCCAAAAGAAACCTTCAAAACCATGCAA 24596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9851 GGATTCCTGGGCTCAAGCAATCCTCCTGCCTCAGGCAA 9814
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27; Conserv
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Pred. No. 1.7e+02;
0; Mismatches 11; Indels 0;
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0; Mismatches 11;
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, NAME/KEY: misc_feature

; LOCATION: (1).\(\tau\). (126200)

; OTHER INFORMATION: n = A,T,C

US-09-949-016-13193
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                                                                                                                                                                                                                                                                                        Sequence 5. Application US/0; Patent No. 6465217; GENERAL INFORMATION: APPLICANT: Boyes, Douglas APPLICANT: Woessner, Jeffr APPLICANT: Gorlach, Jorn
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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Best Local Sim
Matches 27;
            SOFTWARE: PatentIn version 3.0 SEQ ID NO 5 LENGTH: 5099
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13193
LENGTH: 126200
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Best Local
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                                                                       CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
                                                                                                                                 FILE REFERENCE: 9128.14
                                                                                                                                                APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS
TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
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ORGANISM: Human
TYPE: DNA
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Hoffman, Neil
Kloti, Andreas
Zayed, Adel
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Gorlach, Jorn
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71.1%;
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Pred. No. 1.9e+02;
0; Mismatches 11;
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Pred. No. 1.9e+02;
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CURRENT APPLICATION NUMBER: US/10/267,763
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 09/610,040
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 5099
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(5099)

OTHER INFORMATION: n = A,T,C or
US-10-267-763-5
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US-09-949-016-88655
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Sequence 88655, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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Best Local Similarity 88.0%;
Matches 22; Conservative
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APPLICANT: Gorlach, Jorn
APPLICANT: Boyes, Dougle
APPLICANT: Davis, Keith
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Best Local (
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TITLE OF INVENTION: MSTHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: MODULATION OF CHORISMATE SYNTHASE AND CHORISMATE MUTASE
TITLE OF INVENTION: EXPRESSION OR ACTIVITY IN PLANTS
FILE REFERENCE: 2035DIV1
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LOCATION: (4049)..(4049)
OTHER INFORMATION: "n" indicates any nucleotide (A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
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22; Conserv
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Davis, Keith
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Woessner, Jeffrey
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ilarity 88.0%;
Conservative
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Pred. No. 1.1e+02;
0; Mismatches 3
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Pred. No. 1.1e+02;
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APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CTEPB
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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US-09-620-312D-22
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                                                                                                                                                                                                                                                       SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 22
LENGTH: 2615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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SOPTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 88655
LENGTH: 601
TYPE: DNA
                                                                         Matches
                                                                                      Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (160)..(849)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
1855 ATACCAGTTCCCAAACAAACCATCTCTCCATTGGAA 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 GTATAAGTWCTCCCAAACGTTGCTTCTTAATAATAAAA 330
                                                                       26;
                     4 ATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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Asundi, vi...
Zhang, Jie
Zhang, Felyan
Chen, Rui-hong
Chen, Qing A.
Thao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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Wang, Dunrui
Wang, Zhiwei
Wang, Tillinghast
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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                                                                       Conservative
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                                                                                    50.0%;
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Pred. No. 79;
1; Mismatches
                                                                                      Score 20; DB 4;
Pred. No. 1.1e+02;
                                                                     Mismatches
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                                                                                                        Length 2615;
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                                                                     Gaps
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Search completed: September 15, 2005, 08:25:23
Job time : 7.05048 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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24: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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10230.248 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0 144000	Result
44444 000004	ult No. Score
100.0 100.0 100.0	Query Match
	Query Match Length DB
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US-10-713-381-6 US-10-713-381-5 US-10-713-381-3 US-10-713-381-9 US-10-713-381-1 US-10-713-381-1 US-10-713-381-2 US-10-713-993-6880	DB ID
Sequence 6, Appli Sequence 5, Appli Sequence 3, Appli Sequence 9, Appli Sequence 1, Appli Sequence 2, Appli Sequence 6880, Ap	Description

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10 18 22 22	13 14 15		15 14 15	16 18 18 18 18 18 18	18 13 13 11 11
229	-10-027-632-1 -10-027-632-1 -10-239-676-1 -10-240-453-2	-09-997-722-205 -10-087-192-178 5-10-027-632-7621 5-10-027-632-7621 -10-437-963-4616	-10-473-126-34 -10-311-455-15 -10-221-714A-2 -10-239-676-13 -10-240-453-21	S-10-240-452-4 S-10-240-454-29 S-10-210-454-29 S-10-312-841-1 US-10-312-841-2 US-10-311-841-2 US-10-424-599-20 S-10-424-599-20 S-10-260-238-25 S-10-260-238-25 S-10-261-318-36	US-10-424-599-31006 US-10-425-115-143168 US-10-425-115-143169 US-10-087-192-1948 US-10-087-192-1948 US-10-473-126-342 US-10-417-455-277 US-09-938-842A-1555 US-09-938-842A-1555
Sequence 4, Appli Sequence 91073, A Sequence 170, App Sequence 178, App	equence 1 equence 1 equence 2	equence 205, equence 178, Sequence 7621 Sequence 7621 equence 4616,	156 222 13,	4; PF 901, 23, F e 1, F e 2, F 24043 20320 20320 2594, 361,	Sequence 31006, A Sequence 83179, A Sequence 83179, A Sequence 1948, Ap Sequence 342, App Sequence 277, App Sequence 1555, Ap Sequence 1555, Ap Sequence 1555, Ap

ALIGNMENTS

RESULT 1 US-10-713-381-6

Sequence 6, Application US/10713381 Publication No. US20040221331A1

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GENERAL INFORMATION:

APPLICANT: ALBERTSEN, MARC C.

APPLICANT: GCX, TIMOTHY W.

APPLICANT: GCX, TIMOTHY W.

APPLICANT: GCX, TIMOTHY W.

APPLICANT: COX, TIMOTHY W.

APPLICANT: KENDALL, TIMOY I.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R

CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT APPLICATION NUMBER: 08/880,499

PRIOR APPLICATION NUMBER: 08/880,499

PRIOR APPLICATION NUMBER: 08/880,499

PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 40

TYPE: DNA

ORGANISM: Zea mays

US-10-713-381-6

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 40; Conservative 0; Mismatches 0; Gaps 0;
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AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC

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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/80,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 158
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RESULT 4
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Best Local S
Matches 40
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
                                                                                                                                                           Query Match
Best Local S
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SEQ ID NO 5
LENGTH: 50
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                                                                                                                                        Matches
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
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FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-1
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; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9
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US-10-713-381-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 40; Conserv
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Publication No. US20040221331A1
GENERAL INFORMATION:
                                                                                    Matches
                                                                                                    Query Match
Best Local Similarity
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Publication No. US20040221331A1
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT FAPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR PELING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
  1239
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                               AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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                                                                                  100.0%; Score 40; DB 20; ilarity 100.0%; Pred. No. 6.4e-06; Conservative 0; Mismatches 0;
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ilarity 100.0%;
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Pred. No. 4.6e-06;
0; Mismatches 0;
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US-10-713-381-2
; Sequence 2, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:

APPLICANT: ALBERTSEN, MARC C.

RESULT 6

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; Sequence 31006, Application US/10424599
; Publication No. US20040031072A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6880
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Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                          GENERAL INFORMATION:
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Best Local
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
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APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL001496
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TYPE: DNA
ORGANISM: Zea mays
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OTHER INFORMATION: n =
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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HUFFMAN, GARY
KENDALL, TIMMY L.
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; Pred. No. 38;
0; Mismatches
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Pred. No. 6.4e-06;
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US-10-424-599-83179
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US-10-425-115-143168
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US-10-425-115-143168
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                                                                                                                          Sequence 83179, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
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TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
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SEQ ID NO 143168
LENGTH: 294
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SEQ ID NO 31006
LENGTH: 706
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Best Local
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yonqwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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ORGANISM: Zea mays
FEATURE:
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ORGANISM: Glycine
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_46127C.1
                                      FEATURE:
                                                              ORGANISM: Glycine max
                                                                                                        TYPE: DNA
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Pred. No. 45;
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Pred. No. 31;
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; ORGANISM: Homo sapiens
US-10-087-192-1948
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                                                                                                                               US-10-473-126-342
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SOFTWARE: FABELSEQ for Windows Version 4.
TOWNSDER OF 1948
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Matches 26
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                          SEQ ID NO 342
LENGTH: 4110
                                                                                                                                                                                                                                                                                                                                                     Sequence 342, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
                                                              Matches
                                                                              Best Local
                                                                                             Query Match
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
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CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
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                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                           OTHER INFORMATION: chemically treated genomic DNA
                                                                                                                                                             FEATURE:
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                              4 ATACCTACTCCCAAACAATCCATCTTAC 31
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AMACCTAMCCCCAMACAMTCCATCCTAC 3056
                                                                                                                                                                                                                                                                                                                                                                      Application US/10473126 o. US20040234973A1
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Pred. No. 2e+02;
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Pred. No. 59
                                                                              Score 21.6; DB 21
Pred. No. 1.9e+02
                                                              Mismatches
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                                                                                             DB 20;
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT PILICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1555
LENGTH: 1341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-277
                                                                                                                                                                        US-09-938-842A-1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-842A-1555/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/ED01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424

SEQ ID NO 277
LENGTH: 6309
TYPE: DNA
Application Statistical Common
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Best Local Similarity 75.0
27; Conservative
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APPLICANT: OLEK, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 277, Application US/10311455 Publication No. US20030143606A1
                                                                                      Matches
                                                                                                                             Query Match
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                                                                                                          Best Local Similarity
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                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3335 ATACCTATTCCCATACGACCAATCTCAATAATCCAA 3300
288
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                           AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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71.8%;
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Pred. No. 1.9e+02;
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Pred. No. 2.1e+02;
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RESULT 13

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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEG ID NOS: 5379
SEQ ID NO 1555
LENGTH: 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-938-842A-1555/c
; Sequence 1555, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
Search completed: September 15, 2005, 20:46:11 Job time : 32.0505 secs
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                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1555
                                                                                                                                                                                                    Query Match 53.5%; Score 21.4; DB 11; Length 1341; Best Local Similarity 71.8%; Pred. No. 1.9e+02; Matches 28; Conservative 0; Mismatches 11; Indels 0;
                                                                                                        288 AGTCCACCTATTCCCAAACAATCTCTGTGCCTCACACAA 250
                                                                                                                                         1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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Post-processing: Minimum Match 0%
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Listing first 45 s
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gb_est6:*
gb_est6:*
gb_gss1:*
gb_gss2:*
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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AQ321478	BX036329	AZ021739	BX036328	BX047050	CG982704	BX071651	•	CL084441	CG383910	CG811817	CK949745	BM027586	AI382034	BF601210	AI467879	AA725064	AI698201	AI206216	CN317130	(201,007)
RPCI11-10	Single re	RPCI-23-3	Single re	Single re	CH240_164	Single re	p3fmgcf_0	ISB1-3G16	OGZAP61TV	FSAAM35TR	4074916 B	GIT000109	te33g05.x	266128 MA	tj78e09.x	ai06h07.s	wa67g11.x	qr27f06.x	AGENCOURT	MODIFICOOKI

TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1 CC656939/c LOCUS 밁 Ś ORIGIN ORGANISM FEATURES DEFINITION Query Match 100.0%; Score 40; DB 9; Best Local Similarity 100.0%; Pred. No. 3.2e-05; Matches 40; Conservative 0; Mismatches 0; source 337 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 298 1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40 hitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002) Other_GSSs: OGWDQ20TM Zea mays Zea mays CC656939 OGWDQ20TV ZM_0.7_1.5_KB genomic survey sequence. CC656939 Class: sheared ends. Location/Qualifiers 9712 Medical Center Drive, Tel: 301-838-5843 Fax: 301-838-0208 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. Seq primer: TF Email: whitelaw@tigr.org CC656939.1 GI:32060231 Contact: Cathy Whitelaw /db_xref="taxon:4577" /clone="zyMyBMa0554D15" /clone_lib="ZM_0.7_1.5_KB" /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library" /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" . . 687 687 bp DNA linear GSS 19-JU Zea mays genomic clone ZMMBMa0554D15, Rockville, MD 20850, USA 0; Length 687; Indels GSS 19-JUN-2003 ç, Gaps 0

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SOURCE
ORGANISM
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AUTHORS
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CC656933
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JOURNAL
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                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 963)

1 (bases 1 to 963)

1 (bases 1, to 963)

2 (bases 1, to 963)

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9 (ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGWDQ20TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence.
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1 (bases 1 to 915)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Whitelaw,C.A., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
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Zea mays
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Fax: 301-838-0208
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Other_GSSs: OGWDQ20TV
                                                                                                                                                                                                                                                                                                                                                                                                               CC656933.1 GI:32060225 GSS.
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Other_GSSs: OG1AG08TH
                                                                                                                                                                                                                                                                                                                                                Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="ZMMBMa0716B15"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/mol_type="genomic D
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estewatson.wustl.edu
Insert Size: 1161
High quality sequence stops: 349
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
Seq primer: M13RP1
High quality sequence stop: 349.
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1 (bases 1 to 528)

1 (bases 1 to 528)

1 (bases 1, to 528)

2 (bases 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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Class: sheared ends
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Fax: 301-838-0208
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Location/Qualifiers
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
/dev_stage="73 days post natal"
/lab_host="DH108 (ampicillin resistant)"
/clone lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:424875"
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/mol_type="genomic DNA"
/strain="B73"
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Pred. No. 3.4e-05;
Mismatches 0;
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RESULT 6
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AUTHORS
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BZ706605/c
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Matches 29
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Best Local Similarity
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                                                          255 GGATATCTACTTGTGAACCATACATTTTACTNAAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian,Y., Jin,L. and Su,B.

BAC end sequences of spider monkey gunpublished (2003)

Contact: Qian Y, Jin L, Su B.

Center for Genome Information
University of Cincinnati
Kettering Lab, 3223 Eden Ave., Cincinati
Tel: 1-513-558-6678
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BZ706605.1 GI:30843142

GSS.
Ateles geoffroyi (black-handed spider monkey)

Ateles geoffroyi

Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Platyrrhini; Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ706605 375 bp DNA 1
SM416B1-G07_55_13.ab1 Spider Monkey genomic
geoffroy1 genomic, genomic survey sequence.
                                                                                       2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: subn@ucmail.uc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 1-513-558-4505
                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATACCTACTCCCAAACAATCCATCTTACTCATGCA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMATCTACTCTCAMACATTTCATCTTATACATGCA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC ends
                                                                                                                                                                                              /cell type="pibroblast"
/cell_line="AG05352"
/dev stage="3 DA"
/clone_lib="Spider Monkey genomic BAC library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Genomic partially digested with EcoRI, Vector, pBACe3.6; Recombinants were transformed into DH10B. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ateles geoffroyi"
/mal_type="genomic DNA"
/strain="black-handed spider monkey"
/db_xref="taxon:9509"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                            tissue_type="Skin"
                                                                                                                                                                                                                                                                                                                            sex≖"Male"
                                                                                                                                      59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.5%;
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Pred. No. 97;
0; Mismatches
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                                                                                                                                    Score 23.6; DB 8;
Pred. No. 1.1e+02;
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cincinnati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic
                                                           217
                                                                                                                                                   Length 375;
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                                                                                                                       Indels
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BAC library Ateles
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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CR181951
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AUTHORS
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KEYWORDS
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JOURNAL
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                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 ATACACACTCCCATACAACGCAAGTGACTCATGCAA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GR_Eb01H15.r GmRNA sequence.
CO117589
CO117589.1 GI:
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 783) Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                                                                                                                 CR181951 783 bp DNA linear GSS 06-JUL-201 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN361p21, genomic survey sequence. CR181951 GI:49960800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
Fax: 520 621 1259
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (Dases 1 to 738)

Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Widall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
                                                                                 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                            GSS; genome survey sequence; MICER
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01 row: H column: 15.
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/dev_gtage=" 3 to +3 DPA"
/lab_host="DH10B" +3 DPA"
/clone_lib="GR_Eb"
/clone_lib="GR_Eb"
/note="Vector: pCMv.SPORT-6.1; Site 1: NotI; Site 2:
ECORV; Library made by Invitrogen wTth RNA supplied by
Wendle lab. Directional cloned into NotI-Ev. Colonies
plated/picked by AGI. More glycerol clones held in -80."
/organism="Mus musculus"
/mol_type="genomic DNA"
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                                                            Location/Qualifiers
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/clone="GR__Eb01H15"
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/mol_type="mRNA"
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77.8%;
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Pred. No. 1.8e+02
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                                                                                                                                                                van der Weyden,L.,
Nishijima,I., Yu,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 16-JUN-2004
GR__Eb01H15 3',
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JOURNAL COMMENT
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CD495749
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AUTHORS
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CL109241/c
                                                                                           ACCESSION
VERSION
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Best Local S
Matches 28
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CD495749
CD495749.1 GI:31422780
EST.
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                               CD495749 1253 bp mkr
CDA18-D05.yld-s SHGC-CDA Gasterosteus
CDA18-D05 3', mRNA sequence.
                                                                                                                                                                                                                                                 5 TACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence.
CL109241
CL109241.1 GI:40602876
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Sequencing Center
Washington University School of Medicine
Email: submitssions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kremitzki,C., Carter,J., McPherson,J., Warren,W., Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: Sp6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos; Silurana.
                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISB1-51D14_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-51D14,
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                                                                                                                                                                                                                                TACATACTCCCATACAATCCATTTTAATGAAATAAC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence start: 72 quality sequence stop: 524.
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                                                                                                                                                                                                                                                                                          Conservative
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/clone="MHPN361p21"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                  Library Segment
                                                                                                                                                                                                                                                                                                                                                                    (clone_lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
/ibrary Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db xref="texoon.8364"
/clone="ISB1-51D14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1018
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Pred. No. 1.9e
0; Mismatches
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Pred. No. 1.8e+02;
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.9e+02;
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                               Euteleostomi;
                                                                                                                                                     EST 12-JUN-2003
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                  Neoteleostei;
                                                                                                                                      clone
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AZ883408/c
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Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) Other_GSSs: RPCI-23-189L2.TV
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Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
                                                                                                                                                                                                                                                         GSS
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                                                                  Akinret, B., Levins, M., Mcgann, S., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                            AZ883408.1
                                                                                                                                                                                                                                                                                                                         genomic survey sequence
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Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gasterosteidae; Gasterosteus.
1 (bases 1 to 1253)
                                                                                                               Zhao, S., Nierman, W., Feldblyum, T.,
                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 405)
                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                               Mus musculus (house mouse)
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Fax: 650 725 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kingsley, DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kingsley, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence start: 15 quality sequence stop: 667 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /notes Tvector: lambda ZAP Express/pBK-CMV; Site 1: EcoR1 (5' adaptor); Site 2: XhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoR1 cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mixed male and female"
/tissue_type="heads and inte
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Salinas river,
/db_xref="taxon:69293"
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                                                                                                                                                                                                                                                                                                                                     musculus genomic clone
                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                        Tsegaye, G.,
                                                                                                               Malek,J.,
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                                                                                                             Shatsman, S.
                                                                                        Geer, K.,
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RPCI-23-189L2,
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                                                                                          Krol,M.,
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BG506830/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 798)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BACpage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 189 row: L column: 2
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG506830.1 GI:13468347
EST.
                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: L/LCM916 row: e column: 11 High quality sequence stop: 2.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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/clone lib="RRCI-23"
/clone lib="RRCI-23"
/clone lib="RRCI-23"
/clone lib="RRCI-23"
/clone lib="RRCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="RPCI-23-189L2"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                             Location/Qualifiers
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s cDNA clone
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  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM9274 row: k column: 01
High quality sequence start: 3
High quality sequence stop: 648.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 968)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           968 bp
601789606F1 NCI_CGAP_Lu30 Mus mu
mRNA secuence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF143726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF143726.1 GI:10982766
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/clone="IMAGE:4071154"
/lab_host="HH108 (T1 phage-resistant)"
/clone lib="NIH_MCC_77"
/clone lib="NIH_MCC_77"
/clone lib="NIH_MCC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                           /lab host="univ"
/clone_lib="NCI_CGAP_Lu30"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
/site_2: SalI; transgenic model WNT-1, expression driven by
/MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
/mTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
dT. Library constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                           /tissue_type="tumor, metastatic to mammary"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:4020600"
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57.5%;
74.4%;
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Pred. No.
Score 23; DB 2;
Pred. No. 2.3e+02;
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musculus cDNA clone IMAGE:4020600 5',
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2.2e+02;
5;
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AUTHORS
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AW257178
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BM406466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: potato-array@tigr.org
This clone can be obtained from the University of
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.
                                                                                                                                                                                                                                                                                                             27;
Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
                                                                                                       sequence.
AW257178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Robin Buell
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ror Tanksley,S. and Baker,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end, mRNA sequence.
BM406466
BM406466.1 GI:18258084
EST.
                                                                     AW257178.1 GI:6605435
EST.
                                                                                                                                       EST305315 KV2 Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asterids; lamiids; 1 (bases 1 to 771)
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                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="potato roots" /clone lib="potato roots" /clone lib="potato roots" /clone | LeorI; Site 2: /notes"vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="Kennebec"
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lab_host="SOLR"
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clone="cPRO27F14"
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2.6e+02;
nes 7;
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KV2-7D15, mRNA
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CPRO27F14 5'
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VandenBosch, K., Endre, G.,
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VandenBosch, K., Hurt, J.,
Town, C.D., Bowman, C.L., (
Fraser, C.M.
Department of Plant Biology University of Minnesota
                                                                                                                                                                                                                                                                                                                           BE205271 560 bp
EST397947 KV0 Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kvandenb@cbs.umn.edu
Texas A&M EST name:T11883e
TIGR sequence name:MTAAO20TK
More information is availble at. (and for
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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University of Minnesota
220 BioSci Center, 1445 Gor
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Contact: VandenBosch K
                                                                                   Town, C.D., Bowman, C.L., Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 612 624 2755
Fax: 612 625 1738
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/mol_type≃"mRNA"
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/db_xref="taxon:3880"
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86.2%;
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Pred. No. 2.8e+0
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Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Burmatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Toreids; eurosids; eurosids; Fabales; Fabaceae; Papilionoideae; Trifolieae;
ESTs from uninoculated seedling roots of Medicago truncatula Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="KV2"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was prepared ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."
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                                                                                                                    ., Hur,J., Moore,J., Beremand,P., Ellis,L., Craven,M.B., Hansen,T.S., Holt,I.E. and
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pKV0-21I23, mRNA
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,, Holt,I.E. and
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Search completed: September 16, 2005, 08:08:43
Job time : 124.754 secs
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA Fax: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
Texas A&M University name:T265043e
TIGR sequence name:MTGBK60TK
More information is available at.
http://chryste.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                    ACCAACTCCCAAACAATCAATCGTGCTCA 52
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV0-21123"
/tissue_type="Seedling roots"
/tissue_type="Seedling prior to inoculation with
/dev_stage="Immediately prior to inoculation with
Sinorhizobium mediloti (0 hour)"
/lab_host="E.coli strain XLOLR"
/clone_lib="KV0"
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/Clone lib="KVO"
/note="Vector: pBluescript SK -; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
Was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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86.2%;
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Pred. No. 3e+02;
0; Mismatches 4;
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Post-processing: Minimum Match 0%
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AX224394 LOCUS 밁 S ORIGIN FEATURES Query Match 100.0%; Score 1311; DB 6; Best Local Similarity 100.0%; Pred. No. 3.6e-252; Matches 1311; Conservative 0; Mismatches 0; source Zea mays Zea mays Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 1 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) AX224394 1394 bp Sequence 1 from Patent WO0160997. AX224394 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. AX224394.1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60 /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" GI:15554636 DNA Length 1394; Indels 0; linear and Kendall,T.L. of using same PAT 10-SEP-2001

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Male tissue-preferred regulatory region and method of using sai Patent: JP 2001520523-A 1 30-OCT-2001;
PT PATENT HERED INTERNATIONAL INC
PN JP 2001520523-A/1
PD 30-OCT-2001
PF 19-UN-1998 JP 1999504910
PF 22-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMA PI TIMMY L KENDALL
PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC C07K14/34,C1201/68,
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                                                                                                                                                                                                                    BD062176 1394 bp DNA linear PAT 27-AUG-2002 Male tissue-preferred regulatory region and method of using same. BD062176 GI:22607781 pg 2001520523-A/1. Homo sapiens (human)
                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhin: 1 (bases 1 to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Kendall,T.L.
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/mol_type="genomic DNA"
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1021 TTCTCTAGATTAGTAAAAGGGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC 1080	781 TITCTGATITITIAAGAGCTAGTITGGCAACCCTGTTTCTATAAGAATITTGATITT 840 [CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120

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al Similarity 100.0%; Score 1311; DB 8; Length 3343; al Similarity 100.0%; Pred. No. 3.5e-252; 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	/codon_start=1 /product="male fertility protein" /protein id="AAKS2489.1" /protein id="AAKS2489.1" /db_xref="GI:14028757" /db_xref="GI:14028757" /translation="MEKRULQWRRGRDGIVQYPHLFFAALALLIVADPFGLSPLAEV /translation="MEKRULQWRRGREFTGEVGEVFGPESIEFDLQGRGPYAGLA DGRVVRWMGEBAGWETFAVMNPDWSEEVCANGVNSTTRKQHEKEEFCGRPLGLRFHGE TGELYVADAYYGLMVVGGSGGVASSVARBADGDE IFPANDLDVHRNGSVFFTDTSMRY SRXDHLMILLEGEGGRALLRYDETSGYHVVLKGLVFPMQVQISEDHGFLLFSTTNC RIMRYWLEGPRAGEVEVFANLPGFPDNVRSNGRGQFWVAIDCCRTPAQEVFAKRPWLR TLYFKFPLSLKVLTWKAARRMHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK LWIGTVAHNHIATIPYPLED"	/gene="M845" join(<1392. 1768,18982182,22802447,2534>2942) /gene="M845" /product="male fertility protein" join(13921768,18982182,22802447,25342942) /gene="M845"		Pox.T.W., Trimnell,M.R. and Albertsen,M.C. Cloning of M845, a gene required for male ferility from Zea mays Unpublished 2 (bases 1 to 3343) Pox.T.W., Trimnell,M.R. and Albertsen,M.C. Direct Submission Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50.31-1004, USA Location/Oualifiers	AF360356.1 GI AF360356.1 GI Zea mays Zea mays Zea mays Zea mays Zea mays Clade; panicoi I (bases 1 tc	1141 GGTTCGGCAGCTCTCGTGTCAACATGCATACTACATGCTTGTTCAACCGTTCGTC 1200 1201 TTGTTCGATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260
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1021 TTCTCTAGATTAGTAAAAGGGAGAGAGAGGAAGAAATCAGTTTTAAGTCATTGTCCC 1080	841 TTCAAAAAAATTAGTTTATTTTCTCTTTTATAAATAGAAAACACTTTAGAAAAATAGAGT 900	ATGACTATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCAAAGAATC 78 TTTCTGATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTCTTCTTCAAAGAATTTTTTTT	601 TRATATCGAAAGGTAAGGTAAGCTTTCAGATTTTTCTTTTTTTT	481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540	361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420	121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCCGGTTGCTCCAT 180

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REFERENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albertsen, M.C., Pox, T.W., Garnaat, C.W., Huffman, G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 9 23-AUG-2001, PIONBER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                              Male
                                                                                                                                                                          clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                               Zea mayв
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                            Albertsen, M.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTTCCTGAAC 1311
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                                                                                          tissue-preferred regulatory region nt: WO 0160997-A 3 23-AUG-2001; EER HI-BRED INTERNATIONAL, INC. (US)
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3 from Patent WO0160997.
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             /mol_type="unassigned DNA"
/db_xref="taxon:4577"
                                                                           Location/Qualifiers
                                          organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/mol_type="unassigned
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97.6%;
                                                                                                                                            Fox, T.W., Garnaat, C.W.,
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Pred. No. 5.9e-22;
0; Mismatches 4
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                                                                                                                                            Huffman,G.
                                                                                                                              and method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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l of using
                                                                                                                           and Kendall, T.L. of using same
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AUTHORS
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AC147602
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., MacCdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macddonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macddonald, P., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tawers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submitseion

Submitted (19-DBC-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Sirren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.,
Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S.,
Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S.,
Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P.,
FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L.,
Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Jones,C., Kamat,A.,
Major,J., Manning,J., Mabbitt,R., MacLean,C., Macdonald,P.,
Major,J., Manning,J., Matthews,C., McCCarthy,M., Meldrim,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1274
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Birren,B., Nusbaum,C., Lander,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE2;
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HASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
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Pred. No. 5e-19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                       Bharti, A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bharti, A.K.
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COMMENT

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source
                                                                                                                                                                                                 is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
100617: contig of 100617 bp in length
100718 100717: gap of unknown length
100718 104370: contig of 4013 bp in length
104731 10430: gap of unknown length
104731 10430: gap of unknown length
115105 115204: gap of unknown length
115205 156396: contig of 41192 bp in length
115205 156396: gap of unknown length
115497 179336: contig of 41927 bp in length
115497 17936: contig of 6163 bp in length
119337 180199: contig of 6163 bp in length
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Wyman,D., ive-
'rect Submission
''7-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 17, 2004 this sequence version replaced gi:49658659. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Travers, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., VO, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., VO, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., VO, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., VO, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., VO, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wassiliev, H., Venkataraman, V.S., Venkataraman, V.S., Venkataraman, V.S., Venkata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bharti AK and Messing, J: The Plant Genome Initiative Rutgers, Waksman Institute, Rutgers, The State University of Jersey, 190 Freilinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.broad.mit.edu/annotation/plants/maize/randomclones.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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                                                 /organism="Zea mays"
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                                                                                                                                                           Location/
type="genomic DNA"
                                                                                                                                                           'Qualifiers
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162177 TTTCCAAACTAACCCTCAAGTATATAATGAATGCAGGACAA 162217
                                                                                                                                                                                                                                                                                                                                                               Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Feb 21, 2004 this sequence version replaced gi:19570016, gi:20087114.

CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 25769)

Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Elehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum chromosome AX4, complete sequence. AC117267 AC115597
                                                                                                                                                                                                                                                                                                                           (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 25769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence and analysis of Nature 418 (6893), 79-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Noegel, A.A.
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                                                                                                                                                                                                                                                                                                    (http://www.uni-koeln.de/dictyostelium/project.shtml
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                                                                                                                                                                                                                                                            Deutsche Forschungsgemeinschaft
                                        complement (join (832..107 1896..2053, 2231..2360))
/note="GeneID exon scores (in order of location ranges):
23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
                                                                                    /map="5836255-5862024"
                                                                                                        /db_xref="taxon:44689"
/chromosome="2"
                                                                                                                                                                                                                                       Location,
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                                                                                                                                                                                              organism="Dictyostelium"
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                                                                                                                                                                        _type="genomic DNA"
                                                                                                                                                                                                                                   /Qualifiers
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Pred. No.
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                                                             .1070,1237. .1349,1533. .1798,
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2 map 5836255-5862024 strain
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CDS

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complement(5711. .6796)
/note="GeneID exon scores (in order of location ranges):
68.61 - GSCJ_ID dd_00752"
/codon start=1
/product="similar to Plasmodium falciparum (isolate 3D7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSSKGFBAVLDILDTAGGEEYSAMRDQYVRTGÖDFMIVESIDSRSSFEEVGOLK
QHIERVKDRDDVPIIIVGKVDLESRRQVSRIEADQLARSLVPYIETSAKTRSNIEE
AFFILVRHTPRNTVYKVVVMGGGVGKSAIILOFIQNIEVEEVDPTIEDSYRKQVTIS
GLPPIGGSLNKKGSSSSSSSSSGKTGLFNKIFSGKDKQPSPQQAASPSTIDRTGQI
STNRLEANVLSYSMSNLSKEVPLITGDCYYCQGCNVILSRFSNLWKTGDDSFTMKCEF
CKYSNSNILLEQGEIPMKOSUYEVLSSPSTSSTTDGKTKEESIIIYCIDVSGSMGTF
CKYSNSNILLEQGEIPMCSUFYTGSFTSFTDGSKAEESIIIYCIDVSGSMGTF
EVPSLQSEMVNAKKGVKGASSGPSYISRLECVQSSIPTMIDRLSIQYPNKRVVLYTFS
                                                   /translation="MEEKIKFYFEIIDFQNQKFKIQEFTSKLIGLKEESFTTFKPIVY
EKYLNWTQSIEESILKTNGTINKSIFEEIFSYCGYIGEFLEYEPFIVFLKFTTFGIIL
DDYIFEKINSLNMKLNEKEKLINSLIYYNNKNENKIGFEFWEIINEFQNFTHKESFQR
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EPVQSTALGPALLVSAAIASQKMLSEVVICTDGVPNVGLGAIEDLPLGPAQEFYEKVT
KLAQNNKTTINIIGISGSHIDLOVIGKVSEQTMONITIIHPLELAREIRKLTQNPWIA
TDVEMSICLHPTLEINKYDSKQGLSRVVKQFPAVNSLTDLTLLYSSRNRRTEFYQIYP
PQIQIKYTKLDGVRCLRVVSAQLQATPDFNTSTSNANISILAMAFTQQAAKIAQQQEY
MESRLHLKAATKLIRSLCNTDEQWEEFYNFEVLREEMEAPLITCIKNKQQRVEKAATD
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23.29 - GSCJ_ID dd_00728"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (10972. .11979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="GeneID exon scores (in order
10.37, 128.60 - GSCJ_ID dd_00729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNSMSPPPKLDKRRFSRDLIPFTIANI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEIQVFYKMKNVHKSFVEGGRKKDISRRKGEAEINKQYYNIKFT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENYDWTGIPFNEKEVEASNNESTEESTLEKEMNKLEISEENENHNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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24.88, 254.96 - GSCJ_ID d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MRLQIILFLSILLIFQLKSTFSSNDISSTILSITPNFNKDYNNQ
ILSKSEMFRSLEYSSNKKVIEBVFDGFNEVIEVIEVIENIKYLYKSKNSKYVGVDFSFSSFCL
NSKENYLEVIKKFSTISKNIKVYPENIWLUISTHENVINSNYLYNKKNIMEYQBLVI
FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENNKDKLFSSLÞFFYLKNIAENQEFEDYY
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/db_xref="GI:42733681"
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CDS

Sgo

Sg

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STYNNNYYNVNNNSLNNSNNADKOKKTITSTSATILIKENVELYNNGNNNILNNKNS
EDILKOKSI KWNKYDGYITRTINRILLLACNSMDLLSDESINGCMVSQQFDFNIVIEK
SLDEFNQFAGLLQVEVLARYEPDVVWKKDGYEFEQSMSIEYLKQQEQSKFVKV
SSTIQFNEKLFSLVYIPFYYTKYEFQNQSFSFFLNSQNGVISATRPEIGLGKIGDFLK
YTQNYFSTLVCNFEPFSKCKGDELAIIDSFKVYNTSSYFLTFSRSSTNFLGSSSIGHL
TIRNNSKSITATLRGQKRRSVQKGNPFSLLPLHERTFSFKGHWCFEIIDGEVNQIDVI
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/db_xref="GI:42733687"
/translation="MFIGEDCNKITNEEECHKSSECIVINYTPCCGEQKWACSKGTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILKNER INGNDGEITTTTTTTTTSÖSSTTIMTTTTTTNGVNDRNYLLFRQVWRNIVIK
TQILFHLELYNIHANKKVELTPIQLUDYKLQSMVLNYHDDDADEDSYDSDI
DDDDSYSDGANCSSSSGSGSDIGSSSNSINNGISNSSSSSILSNSSLLELSMIRVNSL
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SEGLKSIEFEKEYNVIQDRLLPPSISSIRFSYGFNQRIAKGVISDNVISITFGDSFNQ
SLDGNWLFKQLKHLGFEHKFGGTIKMGLPSSLTSLILDFRSYKGVIEIGSIPFGEHFWS
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LDYKFNSCSNGSSISFNIJKSTRAUF
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SSSIVIKCEEQQQQQQQQQQQQQQQQQQQQQQDGFLKSQEFPNLFKNKLYLKDDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdnnnlpqpyfpqsnnycDcddnengndstltiqpkpiapslps
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NTNPCSNVNCPDGFYCECKDGKTAKCVPSGPTQPPKPPVCSLRCPPNHECRFNDQGHQ
CCVKVHHDRCSLRCPHGHECKVDHNGKECCVRSHRPPPPEVCSLRCPPKHECKFDDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSLNPLFITEXINIIDLSHL"

join(16184. .16199,17272. .17613,17707. .19331)

/note="GeneID exon scores (in order of location
0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFNQIIPQGIFIHTKLKSLNFGYHFNQIIPADTLPPTLESLNLGGYNREITVKNDEYD
CYGISNKGGFGSNSSSNFCYGGTNNGLREMLKNTTSLKTLTLNYFNRKIEVGDLPNSI
ESLNLGYHFNQPIGNNYLPKLLKKLFILNSEFNQNISADGCIPFGLQTIYIRNSNMNF
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gnnkfdysiliiiennnniinkdyQfnnnnknsnnniynnnndnnnsiieekdlnkii
                                                                                                                                                                      cress). Putative PREG1-like
/protein_id="AAS38633.1"
                                                                                                                                                                                             /codon_start=1
/product="similar to Arabidopsis thaliana (Mouse-ear
----- botarive PREG1-like negative regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINPREGGNIYQSIKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="hypothetical protein"
/protein_id="AAS38632.1"
/protein_id="AAS3868"
/db_xref="GI:42733688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDQHGKECCVVAHRPPPKCSLRCPPRHECRVNHFGEECCVKVHHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPKHECRINHFGEECCVKSRNDCLTCEDLNCERKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKCCVKIHCDEVCDLDCGRGFECKIRHDGSKCCVRSERPHPPQHEKCNKRCPPGHECK
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SSGSSSGGVSSCSTTHCPEGYHCSMVNDVATCLASTTGGTGLPGTSSSTAGVSSCLTT
LCP1GH1CVEDSNGVNCVPNGGGTSGGSSSTGTSGGHPDPCRDVDCPDGFHCECKDGK
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mold). Hypothetical 97.7 kDa protein"
/protein idd="AAS38630.1"
/db_xref="GI:42733686"
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/note="GeneID exon scores (in ord
2.42, 1565 - GSCJ_ID dd_00727"
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KTIELIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNSNKILSGIYFAHKKSKRY
                                                                                                                         /protein_id="AAS38633.
/db_xref="GI:42733689"
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (21961. .24357)
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                                                                                                                                                                                                                                                                                                                                         note="GeneID exon scores"
| 13.48 - GSCU_ID dd_00724
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.06.68 - GSCJ_ID dd_00725"
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_00727"
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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AF034389/c
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MEDLINE
PUBMED
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Best Local Similarity
Matches 217; Conserv
                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                     Submitted (12-NOV-1997) Molecular Toernooiveld 1, Nijmegen 6525 ED, Location/Qualifiers
                                                                                                                                                                                                          Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 713)
Dechering, K.J., Kaan, A.M., Mbacham, W., Wirth, D.F., Eling, W., Konings, R.N. and Stunnenberg, H.G.
Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasit plasmodium falciparum
Moll. Cell. Biol. 19 (2), 967-978 (1999)
                                                                                                                                                                                                                                                                                                                                                                                               713
Plasmodium falciparum sexual
partial cds.
AF034389
                                                                                                                                   2 (bases 1 to 713)
Dechering, K.J., Kaan, A.M. and Konings, R.N.H.
Direct Submission
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EQQSIEEETFIESSFEETKEVVEEVPFEEQFEILPISIGEETLKEYTSFLSVLSELIV
DMYNDDDKSSTSSQSSSSSSSSSAPSSPKPIKNNDNVTTTTTTTTTTTTTTTSKTATSS
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1. .>713
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/strain="NF54"
                                            /organism="Plasmodium falciparum"
/mol_type="genomic DNA"
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Pred. No. 0.00015;
0; Mismatches 221;
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                                                                                                      Biology, University
The Netherlands
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                                                        DDU86962
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/product="sexual stage antigen"
/protein_id="AAD12581.1"
/db xref="q1:3098291"
/translation="M"
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711. .>713
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537. .710
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537. .>713
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1. .536
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/note="Pf816"
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Escalante, K., Wessels, D., Soll, D. and Loomis, W.F.
Direct Submission
Submitted (27-JAN-1997) Department of Biology, Un
California, San Diego, 9500 Gilman Drive, La Joll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

1 (bases 1 to 3576)
Escalante, R., Wessels, D., Soll, D.R. and Loomis, W.F.
Chemotaxis to CAMP and slug migration in Dictyostelium both depend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on migA, a BTB protein
Mol. Biol. Cell 8 (9), 1763-1775 (1997)
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                                         /gene="migA"
/note="gene inte
/replace="pbsrl
2900. 2997
                                                                                                                                                                          /number=1
951. .128
                                                                                                                                                                                                                                                                                                        ISLNASQSKLSINNATNTTNNNNNNSNNVTNTNNNNIINNNNNNNNNNKQTQSNNNDNKI
LKRYQPRPPQSILFEYSFDFDFKGIIFWISTDGGNEKWSNPHSTSKIKITSSSIDKGN
LYDIVELTPNAFWTKDVPASWVMIDLGPNRTVVPMYYTIRHGLSYKSDSLRTWDFQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  finger
U14556
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="MigA"
/protein_id="AAB47544.1"
/db_xref="GI:1841872"
                                                                                                                   melanogaster BTB
Number U01333"
                                                                                                                                                                                                                                                  TNGEQWTVLKRHTNDPSLNYKYATHSWPVTGCETAFRYFRILQTGKNSNNRNFLVIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="essential for slug migration"
/note="N-terminus of this protein is similar to other BTB
domain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
2998. .>3423
             /number=1
                                                                                                                                             /gene="migA"
/note="encodes
                                                                                                                                                                                                                                      LEIYGELCETNPNPN"
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/gene="migA"
/product="MigA"
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                           'gene="migA"
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                                                      interruption in mutant"
bsr1 external plasmid, approximately 4
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Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 149526 bases at least react for the formula for th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:53850295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX957346.13 GI:54019944
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149526 bp
Danio rerio clone CH211-117K16,
BX957346
                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
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1 (bases 1 to 149526)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
Insert size: 149526; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTAAAAAACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTTTGTTATTGTTTTTATATACATTTTCTTCTTCTTACAATAGAGTGATTTTCTTCCCGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTTCTTTTTCATTCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAAAATAAAAAATAAAAATAAAAATAAAAATAAAAACAAACAAATTAAATTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.48;
                                                                                                                                                                                                                                                                   Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 0.00043;
0; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear HTC
WORKING DRAFT SEQUENCE.
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Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG 08-OCT-2004
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DEFINITION
ACCESSION
                                         rocus
                                                             PFMAL4P1/c
                                                                                  RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                108523 GTTTTAATAGTTAAAA 108508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108763 ATTATACATATTAAAACTCTTATAATGTTAATGTATAATTAACTATTATAATGTTTCA 108704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108943 CCAAAGTACTAATTAGCATTTTTAATGGTTTTATTTTCAGATTTTTTTATTTTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724
PFMAL4P1 347582 bp Plasmodium falciparum MAL4P1. AL034557 AL844503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 149176; 6.5% error; agarose-fp Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality coverage: 12.54x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTTANAGATTTANAAATATTTTAAAACATGTTTTATCACATATAATGACTAAAGAAGA
                                                                                                                                                                                         TCTAGATTAGTAAAAA 1039
                                                                                                                                                                                                                                                                                                                                                        CAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAATTAGTTTATTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAAACAAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.
                                                                                                                                                                                                                                                                        AGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTC 1023
                                                                                                                                                                                                                                                                                                                 TATTATTGCCCTTCATTAGTCATCTTATATTTAAAAAATATTTAAATATATTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                GTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATG
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:right
clone_end:T7
vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-117K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:03115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Danio rerio"
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46.8%;
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Pred. No. 0.00047;
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                                         DNA
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mungall, K., Bówman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamiin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, B., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Oct 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 347582)

Hamlin,N., Pain,A., Berriman,B.,
Harris,B., Harris,D., Lawson,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Sanger Centre, Wellcome Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell, B.G.
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KYKKFCNGNGGNGEKSATENATSREKGKKGDQMEKWICYYDENKEKKYGSDAINFCYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Similar to Plasmodium falciparum variant-specific surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa) fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(35153. .41725,42757. .44124)
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Quail, M.
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EKGLDAEEAKEIKHLROMLEQAGVRDLAAVGGPCTEGGVAEQNTIMDKFLDEELKEAE OCKNCTKAQQEGPGARSADSPAGTEDHPDAEDDDDEDDEDDEDEEEEEEEE PQCKKTVNDILSTDDRTKOVGDCHEKVYGKNGPDWKCGDLTLUDDTKVCMPPRROKCL YYIAHESETKNIETQDDLRDAPIRTAAAETFLSWQYYKIKNGADAKQLDNGTIPEEFL

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                           ATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGA 623
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44.68;
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Pred. No. 0.00055;
0; Mismatches 341;
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Best Local Similarity 39.2%;
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7675 from Patent CQ422641 CQ422641.1 GI:41374870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
Novel genes, compositions, kits, and methods for identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 TTATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                                                                                                                    TANAAATTTTTTNAAAAACTAATTNTÄANNATANTNAATTTTTTNTÄAAAAAANNNAÄÄÄÄ
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                               AATAANTTNAATTTTTTTTAATNAAAAAAAAAAATTTNAAATTTTAANCAANTNTTTTTT
                                                                                          TTAAANNTTTTNTAANTTATTAAACCAAAATTTTTTTTTAAAAAAATTTTTTAAAANTT
                                                                                                                      AACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACA
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                                                          AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTG
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RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit
                                                                                                                                                                                                                                                                      Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: TTCTACGTCCAAATGCATCAAAGA
Primer B: AGGAAACCAAGCCTTATGAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 241)

McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.

MPZ-UCI Joint SNP Discovery
                                            Genomic DNA amplification
                                                                                                                     Amplicon sequencing ABI protocol - us:
                                                                                                                                                                                                             PCR amplification of genomic DNA Template: 50 ng
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BV119878
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PZA01377 CML247
                                                                                                                                                                                                                                                             STS size:
                                                                                                                                                                                                                                                                                                                                                    321 Steinhaus Hall, Irvine,
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brandon S. Gaut
                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                           Protocol
                                                                                                                                                                                               Template:
Primer:
                                                                                     ABI protocol - using d-Rhodamine terminator sequencing ready reaction with ampliTag DNA Sequence ran on ABI 3700 sequencer.
                                                                                                                                                               dNTPs: each 200 uM
Tag Polymerase: RedTag (Sigma)
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                          (Sigma)
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polymerase
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Search completed: September 16, 2005, 03:01:34 Job time : 4401.14 secs
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Best Local Similarity 61.5%;
Matches 112; Conservative
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                                                                                                        ACTGTTAATTTÁGTTCCAÁTATCCÁTCACCAÁGGÁTGGATATCCTÁACCGCÁTATCTTGT
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/clone_lib="Zea mays CML247"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>241
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic D
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/cultivar="CML247"
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1: geneseqn1980s:*
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pred. and is derived No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

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431	8056	9859	9859	8056	346	439	6027	6027	6027	2657	13400	960	883	158	255	1394	1394	1394	1394	Query Match Length		
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Abx44556 Bovine ES	Abzl0100 Haematopo	Ads89440 Oligonucl	Ads89714 Oligonucl	Abz10246 Haematopo	Aai87279 Human pol	Abx35844 Bovine ES	Adk12106 cDNA enco	Abx09935 DNA encod	Aax58751 Maize dul	Aaz10551 DNA seque	Adr04296 Corn FT h	Acn85231 Breast ca	Aall5210 Human bre	Aah76334 Z. mays M		Aah76333 Z. mays M	Aah76332 Z. mays M	Aax07409 Zea mays	Aax07408 Zea mays	Description		

The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile

and infertile plants

New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.

Claim

2; Page 22-23; 39pp; English.

3 X X X	RESULT 1 AAX07408 ID AAX		n 4	4	4					LJ.	က မ			ш	1.3	Ω ω		141	O N	N)	K)	N	6. 1	N)	۸1	Ω N	
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Ms45; male; tissue-preferred; plant tissue; differentiated; WPI; 1999-105628/09. Albertsen MC, 19-JUN-1998; 30-DEC-1998 Zea mays. 23-JUN-1997; WO9859061-A1 Zea mays Ms45 male tissue-preferred regulatory region (PION-) PIONEER HI-BRED INT INC 97US-00880499. Fox TW, 98WO-US012895 Garnaat CW, regulatory region; plant cells; maize; hybrid seed; fertility; ss. Huffman GA, Kendall TL;

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GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
                                                      TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG
                                                                                                         TTCAAAAAAATTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAAATAGAGT
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Pred. No. 1e-269;
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                                            The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45) which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating malze male fertile and infertile plants
                                                                                                                                                                                                                                                                                                                                                                               New nucleic - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ms45; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                       Claim 3; Page 23-24; 39pp; English.
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Query Match Best Local Similarity Matches 1311; Conserv

100.0%; ilarity 100.0%; Conservative 0

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Score 1311; DB Pred. No. 1e-269); Mismatches

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Length 1394; Indels

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                                                 Sequence 1394 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 255
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Pred. No. 1.3e-24;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                        71 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                 DB 5;
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RESULT 6
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ID AAH7
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           AAH76334;
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                                                                                                  CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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RESULT 7
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The presents sequence represents a DNA fragment as the provided supstream of the present sequence represents a DNA fragment as the provided supstream of the present sequence represents a DNA fragment as the provided supstream of the present sequence represents a DNA fragment as the provided supstream of the present sequence represents a DNA fragment as the provided supstream of the present sequence represents a DNA fragment as the provided supstream of the present sequence represents a DNA fragment as the provided supstream of the provided supstream of the presents and the provided supstream of the provided supstream of the presents and the provided supstream of the
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                                                             Human; breast
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                                                                                                                                                                                                                    AAL15210 standard; cDNA;
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                                                                                             expressed polynucleotide
                                                                                                                                      entry)
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99.4%;
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Pred. No. 1.5e
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                                                           cytostatic;
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Best Local Similarity
Matches 237; Conserv
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
09-JUN-2000; 2000US-0211115P.
25-JUL-2000; 2000US-0220534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26799) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 883
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GTTGCCAGACTAGCCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATT
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                                        NNANATTAAAAAATTTATTTTTTTANTTCTATAAATTAAAANAANANNAATAAAATAAT
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                                                                           TTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGA
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Pred. No. 3.4e-
0; Mismatches
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RESULT 8
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Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cyrostatkic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92914 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated polypeptide associated with breast detecting presence of polypeptide in sample, as a
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Rafalski JA, Sakai
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DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated polynucleotide comprising a CC first, second, third, fourth or fifth nucleotide sequence, or their CC complement encoding a polypeptide either having flowering locus T gene CC (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also CC described: (1) a vector comprising the polynucleotide; (3) transforming a cell with the polynucleotide; (3) transforming a cell by CC transforming a cell with the polynucleotide; (4) a cell comprising the recombinant DNA construct; (5) producing a plant comprising transforming to a plant cell; (6) a plant comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (8) an CC construct; (7) a seed comprising a first nucleotide sequence contains at least 30 nucleotides, where the first nucleotide sequence is comprised by another polynucleotide, where the other polynucleotide includes the second, third, fourth, fifth or construct polynucleotide includes the second, third, fourth, fifth or construct polynucleotide includes the second, third, fourth, fifth or consider polynucleotide includes the second, third, fourth, fifth or construct containing a recombinant DNA construct comprising the polypoptide from a cell containing a recombinant DNA construct comprising the polypoptide from a cell containing a recombinant DNA construct comprising the polypoptide from a cell containing a recombinant DNA construct comprising the polypoptide from a cell containing a recombinant DNA construct comprising the polypoptide from a cell containing a polypoptide comprising the polymocleotide sequence. The polynucleotides are useful for floral development, e.g. engineering plant sterility/fertility, cell construct comprision to enhance cell construct construct comprision to enhance cell construct constru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ10551 standard; DNA; 2657 BP
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                                                                09-MAR-1999;
                                                                                                               16-SEP-1999
                                                                                                                                                                                                                                                                                                                                          DNA sequence of the P-Ztap promoter of maize.
                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-1999
                                                                                                                                                                                                       Zea mays
                                                                                                                                                                                                                                                  flower life; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                            WO9946396-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8679 T 8679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8559 ACCATTTTATTTTCAAGAGGTTTTTATTTTATCAAGAAAAATTAGTTCATTTTCTCTTTGG 8618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        871 ТАЛАЛТАGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCAA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; SEQ ID NO 63; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAATAAAAATCCATTAGAAAAATGGGGTTGTCAAACTAGTCCTTATTTAGTTTTCCAT 8678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                          98US-0077277P
                                                                    99WO-US005126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.3%;
73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69.8;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 11
AAX58751/c
ID AAX587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the P-Ztap promoter of maize. It is used to in the method of the invention. The specification describes a method for the production of male sterile plants. The method comprises selective expression of DNA encoding a protein that causes tolerance to glyphosate and application of glyphosate. The method uses two DNA molecules, each coperably linked to a separate promoter, whereby the first promoter functions in plant cells to produce a protein that causes tolerance to glyphosate, and the second promoter functions in plant cells to cause the groduction of a second RNA sequence in a male reproductive tissue. Expression of the DNA promotes tolerance to glyphosate in those tissues in which it is expressed. Expression of the second DNA molecule. By using a gromoter for the second DNA molecule which can inhibit the glyphosate tolerance generated by expression of the first DNA molecule. By using a gromoter for the second DNA molecule which restricts the production of the matisense RNA to only a subset of the tissues which express the first CNA molecule, only the subset of the tissues in which the second DNA molecule is expressed will be susceptible to glyphosate toxicity. In this way, a specific cell type or combination of cell types, depending upon the CC glyphosate to the plant. The methods can be used for producing malecule which restricts by application of cell types, depending the first constants crop outcrossing, and for lengthening flower life. The methods can be used with plants such as corn, wheat, rice, canola, oat, can be selectively allated by application of cell types, alfalfa, carrot, cotton, oilseed rape, sugarbeet, canola, oat, can be selectively allated, oilseed rape, sugarbeet, cotton, oilseed, oilseed rape, sugarbeet, cotton, oilseed, oilseed rape, sugarbeet, cotton, oilseed, oilseed rape, sugarbeet, cotton, oilseed rape, sugarbeet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                 Starch synthase; SSII; DU1; dull1 gene; maize; transgenic plant; ss
                                                                                                                                                                                                                                                                             AAX58751;
                                                                                                                                                                                                                                                                                                                       AAX58751 standard; cDNA; 6027 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2657 BP; 686 A; 611 C; 677 G; 683 T; 0 U; 0 Other;
                       misc_feature
                                                                                                                                                                              Maize dull1 gene encoding starch synthase enzyme DU1
                                                                                                                                                                                                                                16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sunflower, soybean, tomato, cucumber and squash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1A-B; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of male sterile plants using a gene encoding glyphosate tolerance, used for, e.g. production of hybrid seed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     847 AAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM, Fromm ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTAGCCCTAGA 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAATTAGTTCATTTTCCCTTGGGAAAATAGAAATCCCATGGGAAAATGTGGTTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCTTTTAAGGGCTAGTTTGGGAACCACATTT-TTCCAAGGGATTTCAATTTTCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTAGCCCTAAA 2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                             (first entry
                       Location/Qualifiers
1. .1437
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 67.2; DB 2;
Pred. No. 0.00019;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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CC This is the nucleotide sequence of the maize gene dull1 (dul). To CC illustrate the role of the dul locus in starch biosynthesis, a transposon CC tagging strategy was used to isolate the gene and describe its CC Mu transposon, cloning and characterisation of a portion of the dul locus with CM u transposon, cloning and characterisation of a portion of the gene, and CC isolation a near full-length cDNA (the present sequence). The amino acid CC sequence (see AAY0619) deduced from this cDNA indicates that Dul codes CC for a 186 kDa protein extremely similar to potato tuber starch synthase CC for a 186 kDa protein extremely similar to potato tuber starch synthase CC endosperm. The Dul product contains unique sequence features in its N-CC terminus that may mediate direct interactions with other starch biosynthetic enzymes. Mutations within the maize SSII gene affect CC multiple aspects of starch biogenesis by disrupting an enzyme complex CC containing starch synthase(s). The isolated cDNA can be used to provide an enzyme with which to regulate the production of starch, and with which to regulate the production of starch, and with which to produce altered or novel forms of starch, e.g. in transgenic plants. CC production. Claimed expression vectors comprise the cDNA or fragments of it that code for functional portions of DUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding starch synthase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 104-107; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY06199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-327406/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9924575-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= g
/note= "functional
in Claim 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438. .2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "functional
In Claim 15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "functional fragment of cDNA specifically claimed
in Claim 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "functional fragment
in Claim 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120. .5147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369. .1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "functional fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20. .1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note- "functional fragment of cDNA specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment of cDNA specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claimed
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Query Match Best Local Similarity

5.1%; 77.5%;

Score 66.4; Pred. No. 0.

DB 2; 1609 T;

Length 6027; 0 U; 0 Other

Query Match Best Local : Matches

Local Similarity

5.1%; 77.5%;

Score 66.4; Pred. No. 0.

0.00035;

DB 8;

Length 6027;

93;

Conservative

0,

Mismatches

26;

Indels

1:

Gaps

1;

Sequence

6027

ВP;

1800 A; 1177 C; 1441 G;

1609 T; 0 U; 0 Other;

Sequence

B₽;

1800 A; 1177 C;

1441 G;

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RESULT 12
ABX09935/c
ID ABX099
XX ABX099
XX ABX099
XX ABX099
XX ABX099
XX CABX099
XX Starch
KW Starch
KW LINKR;
KW GYANUI
KW WATERT
XX WO2002
XX WO2002
XX HOOMAI
XX HOMAI
XX HOMAI
XX NEW DI
PT COMMUI
XX WPI;
XX NEW DI
PT COMMUI
XX WPI;
XX OFFICE
CC COMMUI
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CC ABSOC
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CC COMMUI
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                                                                               as compared to plants producing native starch or starch produced with native starch synthases. Expression of the starch synthase fusion proteins along with granule bound starch synthase (GBSS) will lead to a modified starch having an altered or improved morphology, retrogradation, waterbinding, or swelling potential of the granules, gel strength, adhesiveness, cohesiveness, hardness, elasticity, increased or decreased granule size, degree of branching, crystallinity, degree of cross-linking, and increased or decreased glucan chain lengths. This sequence
                                                                                                                                                                                                                                                                                                                              The invention describes an isolated DNA molecule encoding a fusion protein consisting of 4 different functional domains selected from glucan association domain (GLASS), linker domain (LINKR), glucosyl transferase domain (GLYTR), and C-terminal end (CTEND) which are operably linked to one another. The DNA molecule is useful for expressing in plants polypeptides including starch synthase enzymes as fusion proteins with improved affinity to starch and modified catalytic capabilities and to the in vivo and in vitro synthesis of glucan chains of modified lengths
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding fusion protein consisting of 4 different functional domains selected from glucan association domain, linker domain, gluctransferase domain, and C-terminal end, useful for producing modifie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Starch; starch bynchese domain; Ghylk; c-ccm.....
granule bound starch synthase; GBSS; morphology; retrogradation;
granule bound starch synthase; GBSs; derphology; retrogradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Page 225-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001US-0279720P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2002; 2002WO-US009574
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                                                                                Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                         The present invention relates to the isolation of a maize gene, dull 1 (DUI), and the polypeptide it encodes. The DUI polypeptide has starch synthase activity, and comprises an N-terminal arm region, a C-terminal catalytic region, and a region of about 900 amino acids terminating with the catalytic region. The C-terminal catalytic region has a catalytic domain comprising alpha-1,4-glycosyltransferase catalytic activity. The dul polymucleotide sequence is useful in producing starch e.g. from a transgenic plant or transfected cell. The present sequence encodes maize
                                                                                                                                    Sequence 6027 BP; 1800 A; 1177 C; 1441 G; 1609 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                              New nucleic acid designated dull1, encoding a starch synthase, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize; dull 1; DU1; starch synthase; alpha-1,4-glycosyltransferase catalytic activity; starch production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1997; 97US-00968467
12-MAY-2000; 2000US-00554467
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77.5%;
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RESULT 14
ABX35844
                                                                                                            CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic cacid linked to a promoter and a 3, non-translated sequence that CC functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3, end of the mRNA molecule; and CC (2) determining a level or pattern of a molecule in a bovine cell or ctissue comprising: (a) incubating a marker nucleic acid (comprising any CC tissue comprising: (a) incubating a marker nucleic acid (comprising any CC complementary nucleic acid molecule obtained from the bovine cell or CC tissue, where hybridisation between the marker nucleic acid and the CC complementary nucleic acid molecule obtained from the bovine cell or CC tissue, where hybridisation between the marker nucleic acid and the CC complementary nucleic acid mentary nucleic acid is predictive of the complementary nucleic acid is used for CC the detection of the complementary nucleic acid is used for CC telegraphy or pattern of the molecule. The LMFD nucleic acid is used for CC determining a level or pattern of a molecule in a bovine cell or tissue. CC is useful for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or CC for genetically improving cattle. The present sequence is one of the CC present sequence acid in the constructs of the constructs acides. Note: The constructs acides acides acides acides in the constructs of the constructs acides. Note: The constructs acides acides acides acides in the constructs of the constructs acides acides acides acides in the constructs of the constructs acides acides. Note: The constructs acides 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX4947, or complements of them. Also included are appearing as ABX34836-ABX4947, or complements of them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification cattle breeding, or for genetically improving cattle.
                                                                    present sequence was not shown in the specification electronic format from the USPTO web site:
                                            seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 1009; 245pp; English
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                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or resemble for the polypeptides have various to the polypeptides are useful in the diagnosis and/or resemble for the polypeptides where the polypeptides are useful in the diagnosis and/or resemble for the polypeptides and may be useful in the diagnosis and/or resemble the polypeptides are useful in the diagnosis and/or resemble the polypeptides and may be useful to the diagnosis and/or resemble the polypeptides and may be useful to the diagnosis and/or resemble the polypeptides are useful to the diagnosis and/or resemble the polypeptides are useful to the diagnosis and/or resemble the polypeptides are useful to the diagnosis and/or resemble the polypeptides and polypeptides are useful to the diagnosis and/or resemble the polypeptides are useful to the diagnosis and/or resemble the polypeptides are useful to the polypeptides are useful 
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                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                                                                   inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                             Sequence 346 BP; 188 A; 22 C; 16 G; 120 T; 0 U; 0 Other;
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                                                   TTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTTATATACATTTTCTTCT
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Search completed: September 15, 2005, 21:33:20 Job time: 635.708 secs

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1311
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1: /cgn2_6/ptodata/1/lna/5A_COMB.seq;*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq;*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq;*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq;*
5: /cgn2_6/ptodata/1/lna/backfiles1.seq;*
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US-08-4817-826B-13
US-09-313-294A-539
US-09-880-499-2
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US-08-880-499-1
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US-09-9713-550-53
US-09-9713-550-53
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US-09-9713-294A-4773
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        Sequence 1, Appli
Sequence 2, Appli
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Sequence 13, Appli
Sequence 137, Ap
Sequence 137, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 53, Appli
Sequence 15129, A
Sequence 1729, A
Sequence 15349, A
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US-08-880-499-1
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29 51.4 3.9 129415 4 US-09-949-016-16997 30 51 3.9 1601 4 US-09-949-016-15635 31 51 3.9 1141 4 US-09-806-708B-22 32 50.6 3.9 11039 4 US-09-902-540-1280 33 50.6 3.9 16573 4 US-09-949-016-14876 34 50.6 3.9 16573 4 US-09-949-016-14164 35 50.4 3.8 731 1 US-08-451-976-2813 36 50.2 3.8 832 4 US-09-621-976-2813 37 50.2 3.8 317366 4 US-09-621-976-2813 38 50 3.8 1392 3 US-09-621-976-16001 38 50 3.8 1392 3 US-09-949-016-16101 40 49.8 3.8 2435 3 US-09-949-016-16110 41 49.8 3.8 265293 4 US-09-949-016-11934 42 49.6 3.8 640681 4 US-09-949-016-16137 43 49.2 3.8 126176 4 US-09-949-016-16137 44 49.2 3.8 126176 4 US-09-949-016-16137 45 47.8 3.6 601 4 US-09-949-016-16137		ი	ი	O			ი		ი	Ω		Ω		ი	n	Ω		
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	25787, F	16138, 7	16137, A	1, Appli	11934, A	16110, A	1, Appli	1, Appli	16001, A	2813, Ap	Appli	14164, A	14876, A	1280, Ap	22, Appl	156535,	16997, A	

ALIGNMENTS

FILING DAIL: CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REGISTRATION NUMBER: 0578 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800 TELEPAX: (515) 248-4844 INFORMATION FOR SED ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1394 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-880-499-1 Query Match 100.0%; Score 1311; DB 3; Length 1394; Best Local Similarity 100.0%; Pred. No. 1.1e-313; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Sequence 1, Application US/08880499 Patent No. 6037523 GENERAL INFORMATION: APPLICANT: Albertson, Marc C. APPLICANT: Fox, Tim W. APPLICANT: Carl, Garnaat W. APPLICANT: Huffman, Gary A. APPLICANT: Kendall, Timmy L. TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AND METHOD OF USING SAME NUMBER OF SEQUENCES: 2 COMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/880,499 FILLING DATE: CONCURRENTLY HEREWITH CORRESPONDENCE ADDRESS: ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., STREET: Box 1000 CITY: Johnston STATE: IOWA COUNTRY: USA ZIP: 50131

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APPLICANT: Albertson, M.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnasi
APPLICANT: Huffman, Gary
APPLICANT: Kendall, Tim
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                                                                                                                                Matches 1311;
                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                   TELEFAX: (515) 248-4844 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 0578 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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STREET: Darwin Building, 7100 N.W. 62nd A
STREET: Box 1000
CITY: Johnston
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                   GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC
                                                                                          TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA
                                                                                                                                                                                                                                             GCCAGCCCCATAAATTATTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020
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                                                                                                                                                TTCTCTAGATTAGTAANAAGGGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC
                                                                                                                                                                   TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC
                                                                                                                                                                                                                     GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020
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GGTTCGGCAGCTCTCGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC
                                                                       TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Pl
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D603
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                            Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08968542C Patent No. 5981728 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word 6.0.1 for Macintosh

CURRENT APPLICATION DATA:

APPLICATION UMMBER: US/08/968,542C

FILING DATE: No. 5981728ember 12, 1997

CLASSIFICATION BODATA:

APPLICATION UMMBER:

APPLICATION NUMBER:

FILING DATE: THORNEY APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      DESCRIPTION: C
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: maiz
TISSUE TYPE: e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Myers, et al.
TITLE OF INVENTION: dull1 Codes For A No.
TITLE OF INVENTION: Synthase
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLCGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: TX
COUNTRY: US
ZIP: 77071
                                                                                                                                                                                                             LIBRARY: maize endosperm cDNA library
LIBRARY: (gtl1
CLONE: pMgf10; pMg6Aa; pMgt6-2M
                                                                                                                                              Local Similarity
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                                                                           792 TTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTTCAAAAAAA 851
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| TAGTITATITICTCTTTATAAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
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8011 Candle Lane
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                                                                                                                          Score 66.4; DB 2;
Pred. No. 2.4e-06;
0; Mismatches 26,
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                                                       -TTCCAAGGGATTTCCATTTTCCAAGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08410784A Patent No. 5912413
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Best Local &
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LENGTH: 6027
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                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
SOFTWARE: PASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,784A
FILING DATE: 24-MAR-1995
CLASSIFICATION BO
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/US98/24225
PRIOR FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Myers, Alan M.
APPLICANT: James, Martha G.
TITLE OF INVENTION: dull1 Coding for a No. 6639125el Starch Synthase and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: D6036PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: cDNA sequence corresponding to the gene encoding OTHER INFORMATION: starch synthase enzyme DU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JAMES, MARTHA G.
TITLE OF INVENTION: ISOLATION OF SUL, A STARCH DEBRANCHING
TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE
TITLE OF INVENTION: SUGARY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02109
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77.5%;
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Pred. No. 2.4e-06;
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US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
        APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NHHI21.001CTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2523 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                  COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
COMPUTER: IBM PC comp.
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION MATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Heine, Ph.D., Holliday C
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: ISU-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
TELEPAX: 617-451-0313
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDLING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2523 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
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                                                                                                                                                                                                                                                                                      SSEE: Knobbe Martens Olson & Bear
T: 620 Newport Center Drive 16th
Newport Beach
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACATTTTTCAAATAAATTAGTTTATTTTCTCTTGA-AAAATAGGAATTTCTCAGAAAA
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Chitnis, Chetan
Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%;
ilarity 71.4%;
Conservative
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                                NIH121.001CP1
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Pred. No. 0.00015;
0; Mismatches 39
                                                                                                                                                                   Version
                                                                                                                                                                                                                                                                                                                           Floor
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TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS: LENGTH: 19124 base pairs

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PATENT NO. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN
                                                                                                              Query Match 4.3
Best Local Similarity 69.0
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 5397
LENGTH: 279
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Best Local Similarity 50.2%;
Matches 141; Conservative
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                                                                                                                                                                     FEATURE:

NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700350078H1
NAME/KEY: unsure
LOCATION: 10, 12, 185-186, 204, 253, 274, 278
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDN HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                           TYPE: DNA
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849 AAATTAGTTTTATTTTCTCTTTAT-AAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAGA 907
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                                                   TTCCTAANGNCCTAGTTTGGAAACCCCCATTTTCCCCACGGGTTTTTCATTTTCCCAAGGG
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                                                                                                              Score 55.8; DB 4;
Pred. No. 0.00031;
0; Mismatches 39;
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                                                                                                                Indels
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RESULT 9
US-08-880-499-1/c
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US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
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; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
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Best Local Similarity
Matches 127; Conserv
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SEQ ID NO 1357
LENGTH: 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)8
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Myxococcus xanthus FEATURE:
                      APPLICANT: Huffman, Gary A.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORPERDANTENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                      APPLICANT: Albertson, I
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garna
APPLICANT: Huffman, Ga
                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                            320
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                                                                                                                                                                                                                                                                                                            TATTTTA 314
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ilarity 51.4%;
Conservative
                                                                                                                                                               Albertson, Marc C.
PIONEER HI-BRED INTERNATIONAL, INC
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Pred. No. 0.00047;
0; Mismatches 120
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                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08880499 Patent No. 6037523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                      APPLICANT: Cari, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
STATE: I
COUNTRY:
ZIP: 501
                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
                                                    CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                      STREET:
                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                        770
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                                                                                 PIONEER HI-BRED INTERNATIONAL, INC. rwin Building, 7100 N.W. 62nd Ave., P.O.
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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1055)
; OTHER INFORMATION: consensus sequence of A.t. and L.a. FAE1 promoters
US-09-806-708B-23
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                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03
                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 23
Query Match 4.2%; Score 55.4; DB 4; Best Local Similarity 22.5%; Pred. No. 0.00065; Matches 182; Conservative 181; Mismatches 430;
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Best Local Similarity 55.8%;
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PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                 LENGTH:
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STRANDEDNESS: single
TOOLCGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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/ 248-4844
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Pred. No. 0.00064;
0; Mismatches 84;
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Sequence 1, Application US/09004056A

Patent No. 6566586

GENERAL INFORMATION:
APPLICANT: Calgene LLC
ITILE OF INVENTION: Plant Expansin Promoter Sequences
FILE REFERENCE: 125
CURRENT APPLICATION NUMBER: US/09/004,056A
CURRENT ETLING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 60034914
UNMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1
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APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
FITILE OF INVENTION: OVARIAN TUMOR SEQUENCES ANI
FITILE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
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US-09-640-173-53
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53, Application US/09640173
Patent No. 6613515
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Best Local Similarity
Matches 155; Conserv
                                                            Matches 139;
                                                                                         Query Match
                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Gossypium
FEATURE:
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LOCATION: (956)
OTHER INFORMATION: unknown nucleotide
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LOCATION: (947)
OTHER INFORMATION: unknown
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ATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATA
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                                                                           Score 55; DB 4;
Pred. No. 0.00056;
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Pred. No. 0.001;
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APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANTION: COMPOSITIONS AND METHODS FOR FILE CONTROL CONTROL OF OVER CURRENT APPLICATION UNMBER: US/09/713,550
CURRENT FILING DATE: 2000-11-14
ANDMER OF SEQ ID NOS: 205
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYDE: DNA
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US-09-713-550-53
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapien
FEATURE:
311
                       932
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                      AAATTACAATCACTGTG 948
                                                                       AAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCAAT
                                                                                                                  CGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAA
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Pred. No. 0.00056;
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APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Fling, Steven P.
APPLICANT: Fling, Steven P.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484CS
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
Search completed: September 15, Job time: 201.304 secs
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Best Local Similarity 43.8%;
Matches 139; Conservative
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 13420,
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-10-425-115-2 -10-425-115-4	-10-425-115-1 -10-425-115-3	-10-425-115-1 -10-473-126-3	425-114-777 425-114-830	09-960-352-10 -10-425-114-2 -10-425-115-1	-10-109-048-11 -10-425-115-41	-10-634-262-1	-10-425-114-1660	-10-425-114-3088 -10-425-115-1493	-10-425-115-1428	-10-425-115-4978	-10-425-115-7531	US-10-425-115-47165 US-10-425-114-24656	-10-425-114-4041	-10-425-115-87	US-10-198-846-6381 US-10-343-477A-63	-10-425-115-522	5-114-	-10-425-114-319	-10-425-115-1428	-10-425-114-17	-10-425-115-5147	-10-425-115-	-10-425-114-32493	US-10-425-115-141826
quence 21012, quence 48324,	equence 15082 equence 30824	equence 1629: equence 386,	equence 777, equence 830,	09, 073, 7793	Sequence 1145, Sequence 41589,	equence 1, Appl	equence 16607,	Sequence 149304,	142853,	Sequence 17816, A	75310,	Sequence 47165, A Sequence 24656, A	4041, A	e 87756,	იი გე	equence 52219,	Sequence 31061. A	e 31957,	equence 14285	e 17816	equence 51470,	equence	equence 32493.	Sequence 141826,

ALIGNMENTS

US-10-713-381-1

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Sequence 1, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREPERED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SQ ID NO 1
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea may8
US-10-713-381-1
Query Match
Best Local Similarity 100.0%; Score 1311; DB 20; Length 1394;
Matches 1311; Conservative 0; Mismatches 0; Gaps 0;
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CURRENT APPLICATION NUMBER: US/10/713,38
COURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
INUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-2
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Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
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Best Local Similarity 100.0%; P
Matches 1311; Conservative 0;
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Pred. No. 5e-275;
0; Mismatches 0;
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Sequence 9, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMYY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PATENTIN VEX. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 255
TYPE: DNA
ORGANISM: Zea mays
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US-10-713-381-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARMAT, CARL W.
APPLICANT: GARMAT, CARL W.
APPLICANT: KENDALL, TIMOTY L.
APPLICANT: KENDALL, TIMOTY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
GTUDEFWT ADDITION TO THE SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 157; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                       1155 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC-TTGTTCCATCGTC
                       1274 GCAACTTCCATGCAAACACGCACATATGTTTCCCTGAAC 1311
                                                                                             1214 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAAACAATCCATCTTACTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1145 CGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGT
 121
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                                                                        CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT
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ilarity 99.4%;
Conservative
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                                                                                                                                                                                                                        Score 146; DB 20;
Pred. No. 7.3e-22;
0; Mismatches 0;
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Pred. No. 6.1e-25;
0; Mismatches 4
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158
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RESULT 5 US-10-425-115-134230

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US-10-425-114-23340
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US-10-425-114-23340
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                                                                                                                                                    Query Match
Best Local S
Matches 95
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION UNMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 23340
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5.222)B
FULE REFERENCE: 38-21(5.222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 134230
LENGTH: 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23340, Application US/10425114 Publication No. US20040034888A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
APPLICANT: Screen, Steve
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: MRT4577_53903C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              912
851 ATTAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAAAA 850
                                                                                                                                                                        Similarity
                                                                   TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA
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                                                                                                                                                      Conservative
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                                                                                                                                                                        5.6%;
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                                                                                                                                                  Score 74; DB 18; Length 320; Pred. No. 4.8e-06; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80.8; DB 20
Pred. No. 3.1e-07;
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; OTHER INFORMATION: US-10-425-115-141826
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; Sequence 141826, Application US/10425115
; Publication No. US20040214272A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16264
LENGTH: 624
TYPE: DNA
CONCENTION OF TABLET CANNERS OF SEQ ID NOS: 73128
                                                                                                                                                       TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(5322)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 141826 SEQ ID NO 141826 LENGTH: 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%;
Best Local Similarity 73.1%;
  Query Match
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Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
                                                                                                            ORGANISM: Zea mays
                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays FEATURE:
                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ATTAGTTTATTTTTCTTTGAGAAAATAGAATTCCCTTGGGAAATTAGAGTTTCTAAACGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA
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                                                               Clone ID: MRT4577_60829C.1
  5.6%;
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Pred. No. 6.7e-06;
  Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
  DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 624;
Length 1326;
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Indels Length 2729;

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Gaps

2345

971

2405

911

2465

851

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Sequence 32493, Application US/10425114

Publication No. US2004003488BA1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILS REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32493
LENGTH: 2445
TYPE: DNA
TYPE: DNA
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US-10-425-115-83293/c
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US-10-425-114-32493
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                                                                                                                                                                                                                        Sequence 83293, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
APPLICANT: LA ROSS, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 73.6%;
                                                                                                                                                                                                                                                                                                                                                                          1743
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                                                                                                                                                                                                                                                                                                                                                                                                               911
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                                                                                                                                                                                                                                                                                                                                                                                                               GCCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAAAATAGAGTTGCCAGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGGAATCCCTTAGAAAAAAATAGTTTCCAAACTAGCCCTAAAAT 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAAAATTAGTTTATTTTCTCTTTATAAAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAGTTCATTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTA 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTAGGGCTAGTTTGAGAACCCCTTTTTTTTCCCAAAGATTTTCATTTTTCAAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAAT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAGTTGGTGGTGCTGGTATTTCACCTTTAACTGTAAGGACTAATTTGGGAACCCA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCT 815
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Pred. No. 2.3e-05;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.6e-05; 0; Mismatches 50;
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; NAME/KEY: unsure
; LOCATION: (1)..(1203)
; OTHER INFORMATION: unsure at all n locations
; PEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_146936C.1
US-10-425-115-51470
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; Sequence 51470, Application US/10425115
; Publication No. US20040214272A1
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; OTHER INFORMATION: Clone ID: MRT4577_175978C.1
US-10-425-115-83293
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322))B
FULE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 51470
LENGTH: 1203
                                                                                                                                                                                                                        Matches 102;
                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 83293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(272
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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                                                    1130 GAAAATTAGTTTATTTTCTCTTGGAAAAATAAAATCCCGTAGAAAAATAGAGTTTCCAA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2344 TGAGTATCATGAGCTAAAATGTAAAAGGGTAAAATCAAATGTTA 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2464 ATATTTCATTTCCCCCTTGAAAAATAGAAATACCTTGGAAAAAAATAGAGTTTCCAAACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2523 TTTAAGGGCTAGTTTAGGAA-CCTCATTTTTCTAGAGATTTCTATTTTTCCACGAAAAA
                                                                                847 AAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGTTGCCAG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852 TTAGTTTATTTTCTCTTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGTTGCCAGACTAG
                                                                                                                                                                          787 ATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            972 AAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 CCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCAT
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                                                                                                                                     ACTITATTAAGGCTAGTGGGGGAA-CATATTTTCCAAAAAGATTTCTATTTTTTTAAA
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76.1%;
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                                                                                                                                                                                                                                         Score 72.4; DB 20;
Pred. No. 2e-05;
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Pred. No. 2.5e-05;
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Indels Length 1203;

1:

Gaps

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1070

ACTAGCTCTAAGAT

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APPLICANT: Zhou, Yihua

APPLICANT: Kovallo, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 17816

LENGTH: 928

TYPE: DN"
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                                                                    ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61761C.1
US-10-425-115-142853
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; OTHER INFORMATION: Clone ID: LIB3075-032-A3_FLI
US-10-425-114-17816
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                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 142853
LENGTH: 1123
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 142853, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 99; Conserv
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Best Local 8
                                                                                                                                                                                                                                                               APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea maye
                                                                                                                               ORGANISM: Zea maye
                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    685 ACCCCTA 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     910 AGCCCTA 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 AATTAGTTAATTTTCTCTTAGAAAAATAAAAATGTCTTGGAAAAATAGAGTTACCAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   804 TTTTTAAGAGCTGGTTTGGCAA-CCTCATTTTTCTAAGGGATTTCTATTTTACTAAGAAA
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 Conservative
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                 5.5%;
78.0%;
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 Mismatches

Score 71.8; DB 20;
Pred. No. 2.7e-05;
0; Mismatches 27;
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Pred. No. 2.4e-05;
0; Mismatches 27;
                                   DB 20;
                                                                                                                                                                                                                                                                                                      and Other Molecules Associated
 Indels
                                 Length 1123;
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7
Gaps
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US-10-425-115-52216
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; OTHER INFORMATION: Clone ID: UC-ZMFLB73238H12_FLIUS-10-425-114-31957
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US-10-425-114-31957
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                  NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 52216
LENGTH: 2537
                                                                                                                                                                                                                                                                               Sequence 52216, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5331)18

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 31957

LENGTH: 2537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 105;
                                                                           TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(5322)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                                           APPLICANT: Kovalic, Dav
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
TYPE: DNA
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Pred. No. 3.9e-05;
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Minimum DB |
Maximum DB |
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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CG034985 PUIGR68TB	CG333929 OG0AD14TV	-	CG201774 PUICH24TB	CL997678 ZMMBHf001		AL175696 Tetraodon	· CC433618 PUHHP17TD	CC630210 OGUCG53TH	CG349565 OG0F183TH	CC630219 OGUCG53TV	CG082135 PUFQX12TD	CG103452 PUJBE19TB	CC400574 PUHLU61TB	CC400575 PUHLU61TD	CC384247 PUHOC67TB	CC439901 PUHRV15TB	CG414922 ZMMBBb029	CG048704 PUILO19TB	CL235046 ZMMBBb057	CG252571 OG4BB05TC		CG224225 OG1AG08TV	CC656933 OGWDQ20TM			

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6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.4	6.4
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CC385881	CG254365	CG246849	CC676387	BZ996930	AL078714	CG221693	CC385762	CL984151	CL996481	CC003943	BZ676889	CG071791	BZ778636	CC613918	CC620594	BZ784278	CC435780	CG102092	CC430754	BZ797976
PUHMJ82TD	OGWFU41TH	OGWAL22TH	OGKAS81TH	PUGIR50TB	Drosophil	OGWMG04TH	PUHFK14TD	O00PHBMMZ	ZMMBH£000	PUDJN65TD	PUBIG17TD	PUJBK02TB	ih02f10.g	OGJAG88TV	OGUCC26TV	DIENVO9ID	PUHSN02TD	PUFYW94TD	PUHEP05TB	PUGBP28TB

ALIGNMENTS

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JOURNAL COMMENT
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AUTHORS
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                   CC656933
OGWDQ20TM ZM 0.7 1.5 KB Z
genomic survey sequence.
CC656933
CC656933.1 GI:32060225
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 963)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGWDQ20TV

Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS.
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Class: sheared ends.
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
69.3%; Score 908; DB 9; Let 100.0%; Pred. No. 7.8e-180; Conservative 0; Mismatches 0;
                                                                                                                                                                /clone="ZMMBMa0554D15"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK:, Site_1: HincII; 0.7-1.5
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                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="genomic DNA"
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/db_xref="taxon:4577"
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Zea mays genomic clone ZMMBMa0554D15,
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                                                                                                            Length 963;
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SOURCE
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Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 915)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Other_GSSs: OG1AG08TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: whitelaw@tigr.
Seq primer: TF
                                                                                                                                      CGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCAGGTTCGGCAGCTCTCGTGTC
                                                                                                                                                                                                                                                                                       TTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAAT
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                                                     ATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCCAAGCCT
                                                                                                                                                                                                      AAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAG
                                                                                                                                                                                                                                                    GTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTT
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/clone="zmMbMa0716B15"
/clone_ib="zM 0.7 1.5 KB"
/note="Vector: DBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/mol_type="genomic D
/strain="B73"
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Pred. No. 7.7e-132;
0; Mismatches 0;
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CC656939/c
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Best Local Similarity
Matches 421; Conserv
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Tel: 301-838-5843
Fax: 301-838-0208
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1 (bases 1 to 687)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)

Other_GSSs: OGWDQ20TM
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CC656939
CC656939.1 GI:32060231
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mayв
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                 GTGCCTACGTCAGGTTCGGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTT 1188
                                                                                  AGTCATTGTCCCTGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAG
                                                                                                                               TATAATTATTTGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCA 1008
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GTGCCTACGTCAGGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTT
                                                               AGTCATTGTCCCTGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAG
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methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
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Pred. No. 1.6e-77;
0; Mismatches 2
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CG252571
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
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                                                                                                                                                                                    TCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCACGAGACGTATCGGG
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/clone | 1bh="ZM 0.7_1.5KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="B73"
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Pred. No. 1.2e-09;
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                                                                                                                                                                                                                                                                                     30;
                                                                                   202
                                                                                                                    290
                                                                                                                                                                                                                                                                                                                    Length 715;
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lone ZMMBMa0809B10,
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DEFINITION

CL235046 967 bp ZMMBBb0575001r ZMMBBb (HindIII)

Zea DNA

DNA linear GS: mays genomic clone

GSS

15-JAN-2004

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RESULT 6
CG048704
LOCUS
                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity
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                                                                  AUTHORS
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                                                                                                                                                             CG048704
PUILO19TB ZM 0.6_1.0_KB Z
genomic survey sequence.
CG048704
CG048704.1 GI:33920884
GSS.
Zea mays
                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 814)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Contact: Bharti, A.K.
Dr.Joachim Messing's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronz Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 967)
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CL235046.1
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Tel: 732 445 3801
Fax: 732 445 5735
                                  Bennetzen, J
                                                                                                                                                 Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZMMBBb0575001 3',
                                                                                                                                                                                                                                                                                                                                                                               GGATATATGTCCCCCACAAT 289
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               Genomics Consortium
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/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII;
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/mol_type="genomic DI
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/cultivar="B73"
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Pred. No. 8.5e-09;
0; Mismatches 30
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aceae; PACCAD
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aceae; PACCAD
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                                                                                                                         Sequencing of the maize Unpublished (2003) Contact: Rod Wing
                                                                                                                                                                                                                                                                            Zea mays
Zea mays
           Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                             Arizona Genomics Institute
University of Arizona
Biological Sciences West, 4
85721-0088, USA
                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 754)
                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
CG414922
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ZMMBBb0290L09.r ZMMBBb Zea mays
                                                                                                                                                                              and Wing, R.
                                                                                                                                                                                             Yu, Y., Kim, H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: whitelaw@tigr.org
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                               CG414922.1
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/clone="Ibh"ZM 0.6_1.0 KB"
/clone="Vettor: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/mol_type="genomic DNA"
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/db_xref="taxon:4577"
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62.7%;
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genomic clone
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Bharti, A.K.,

Messing, J

Tucson,

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Indels

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Gaps

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Best Local Similarity
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CC439901
CC439901.1 GI:30940477
GSS.
Zea mays
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Plate: 0290 row: 1
Seq primer: M13r
Class: BAC ends.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 950)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Whitelaw, C.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                               Other_GSSs: PUHRV15TD
                                                                                                                                                                                                                                                                                                              Maize Genomics Consortium 
Unpublished (2003)
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                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                Bennetzen, J
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ilarity 71.2%;
Conservative
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                                                                                                                                          sheared ends.
Location/Qualifiers
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/db xref="taxon:4577"
/clone="zMMBTa519D06"
/clone 11b="ZM_0.6 1.0 KB"
/clone 11b="ZM_0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
COT selected genomic DNA library"
                                                                                 /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. 98p. mays"
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cultivar="B73"
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Pred. No. 6.4e-08;
0; Mismatches 47;
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                                                                                                                                         714 TTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermatophyta; Magnoliophyta; Liliopeida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 652)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennetzen, J
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/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol_type="genomic Di
/strain="B73"
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Pred. No. 1.1e-07;
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(., San Miguel,P., Ma,J. and
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Matches 163;
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CC400575
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GSS.
Zea mays
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Other_GSSs: PUHLU61TB
Contact: Cathy Whitelaw
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 301-838-0208
Email: whitelaw@tigr.org
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PUHLU61TD ZM_0.6_1.0_KB Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bennetzen, J
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/clone="zxMHBTa480,101"
/clone lib="ZM_0.61.0 KB"
/note="Vector: pCR4-TOFO; Site_1:
CoT selected genomic DNA library"
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/mol_type="genomic D
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Pred. No. 1.1e
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1.1e-07;
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GSS.
Zea mays
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Query Match
Best Local Similarity
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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                PUJBE19TB ZM_0.6_1.0_KB
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Other_GSSs: PUHLU61TD
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1 (bases 1 to 820)
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PUHLU61TB ZM_0.6_1.0_KB
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Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Cathy Whitelaw
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                                                                                                                                          ATTTCAAATTCCACTTTGCAAAATAGTGTCATC
                                                                                                                                                                                                                                                 AAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                      TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
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                                                                                                                                                                                  AATTATTTGGCCAGCCCCATAAATTATTTAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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ведиепсе
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Pred. No. 1.1e-07;
0; Mismatches 109;
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8 Zea mays
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Y., San Miguel,P., Ma,J. and
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                                       GSS 20-AUG-2003
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GI:33985746

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RESULT 13
CG082135/c
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AUTHORS
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Best Local Sim
Matches 116;
                                                                                                                                   TITLE
JOURNAL
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JOURNAL
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TIGR
9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                      CG082135 765 bp DNA linear GSS 20-AU PUFQX12TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0712B24, genomic survey sequence.
CG082135
CG082135.1 GI:33964429
GSS.
                                                                                                                                                                                                                        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                       (bases 1 to 765)

1 (bases 1 to 765)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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                                                                                            Other GSSs: PUFQX12TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
Seq primer: TR
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Other_GSSs: PUJBE19TD
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Unpublished (2003)
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Tel: 301-838-5843
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                                                                                                                                                                                                                                                                                                                          Zea mays
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/clone="lib="ZM_O.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
/COT Belected genomic DNA library"
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/strain="873"
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Pred. No. 2e-07;
0; Mismatches 51;
                                                       Rockville, MD 20850, USA
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CC630219/c
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JOURNAL
                 Query Match
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Best Local Similarity
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1 (bases 1 to 781)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                               Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUCG53TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
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CC630219
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                               sheared ends.
                                                                  /db_xref="taxon:4577"
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methylation filtered genomic DNA librar
                                                                                                                                                                                  /organism="Zea mays"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/clone="ZMMBTa0712B24"
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/mol_type="genomic DI
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Pred. No. 2.2e-07;
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TITLE JOURNAL COMMENT RESULT 15 CG349565/c LOCUS S REFERENCE AUTHORS SOURCE ORGANISM 밁 Ś 밁 Ş ACCESSION VERSION 닭 ક 밁 ORIGIN FEATURES 밁 ঠ S KEYWORDS DEFINITION Query Match Best Local Similarity Matches 125; Conserv Best Local Similarity 71.8%; Matches 125; Conservative **Bource** 907 847 AAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGTTGCCAG 173 907 ACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG 960 847 114 GAAAATTAGTTTATTTTCTCTTGAGAAAATATAAATCACTTGAGAAAATATAGTTTCCAA 787 546 ACTAGCCCTAAAGTATTTTATAAAATAGAGGAAAAATTCGTCTATTTTCATTG 606 GAAAATTAGTTTATTTTCTCTTGAGAAAATATAAATCACTTGAGAAAATATAGTTTCCAA 665 ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGGATTTTTATTTTTTCAAT 787 54 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 815)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics
Unpublished (2002)
Other GSSe: OGOF183TV
Contact: Cathy Whitelaw CG349565 815 bp DNA linear GSS 26-AUG-2003
GG0F183TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0705N21,
genomic survey sequence.
CG349565
CG349565.1 GI:34266831
GSS.
Zea mays
Zea mays 9712 Medical Center Drive, Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org ATTITITAAGAGCTAGTITGGCAACCTGTITCTTTCAAAGAATTITGATTTTTTCAAA 846 AAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAG ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGGATTTTTATTTTTTCAAT 115 ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTTCAAA 846 ACTAGCCCTAAAGTATTTATAAAATAGAGGAAAAATTCGTCTATTTTTCATTG Conservative sheared ends. /organism="Zea mays"
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library" Location/Qualifiers l. .815 6.5%; Score 85.2; DB 9; Pred. No. 2.2e-07; 0; Mismatches 48; Pred. No. 2.2e-07; 0; Mismatches 48; Rockville, 48; 48; MD 20850, USA Length 815; Indels Indels 1; 1; Gaps Gaps 493 906 906 607 55 547

Search completed: September 16, 2005, 08:08:42 Job time: 4089.83 secs

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181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	 121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	Query Match 100.0%; Score 1394; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 0; Matches 1394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577"		FIUNDER HI-BRED INTERNATIONAL, INC. (US) Location/Oualifiers		Male tissue-preferred regulatory region and method of using same		spermacopnyta; мадпотторпуta; ьтторвіda; мовіев; мовсеве; массяв clade; Panicoideae; Andropogoneae; Zea.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Zea mays	Zea mays		AX224394.1 GI:15554636		1 from Patent WOO160997	300 hr DNA linear DAT 10-SED-2001	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Male tissue-preferred regulatory region and method of using same patent: JP 2001520523-A 1 30-OCT-2001;
PALENEL HI BED INTERNATIONAL INC
PN JP 2001520523-A/1
PD 30-OCT-2001
PP 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFWAN, PI TIMMY L KENDALL
PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC ,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
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Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall,T.L.
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Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (Dases 1 to 3343)
Fox, T.W., Trimnell, M.R. and Albertsen, M.C.
Cloning of Ms45, a gene required for male
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Fox, T.W., Trimnell, M.R.
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| Product="male fertility protein" |
| Join(1392. .1768,1898. .2182,2280. .2447,2534. .2942) |
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/mol_type="unassigned
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Male tissue-preferred regulatory region are Patennt: JP 20015205.23-A 2 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC PN JP 2001520523-A/2 PD 30-OCT-2001 PF 19-JUN-1998 JP 1999504910 PF 19-JUN-1997 US 08/880499 PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W PI TIMMY L KENDALL
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Mammalia; Eutheria; Primates;
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Albertsen, M.C., Fox, T.W., Garr
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                                                                                              ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA
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            ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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/mol_type="unassigned
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Pred. No. 1.8e-14;
0; Mismatches 0;
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RESULT 9 AX224399

Bharti, A.K.

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unordered pieces.
AC149836.
AC149836.1 GI:49035067
HTG; HTGS_PHASB1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Zea mays
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Zea maya clone ZMMBBc0496L17,
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Spermatophyta; Magnoliophyta; Liliopsida; Poalea; Poaceae; PACCAD
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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; Pred. No.
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No. 3.4e-09; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Freilinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)

Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 496_L_17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                      35157
                                                                        organism="Zea mays"
                                                                                                                            Location,
                         'mol_type="genomic DNA"
'cultivar="B73"
                                                                                                                 35156: contig of 35156 bp in length 35256: gap of 100 bp 97940: contig of 62684 bp in length 98040: gap of 100 bp 114817: contig of 16777 bp in length acion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T., Lykidis, A., Bhattacharyya, A., Bartman, A., Gardner, W., Grechkin, G., Zhu, L., Vasieva, O., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A., Larsen, N., D'Souza, M., Walunas, T., Pusch, G., Haselkorn, R., Fonstein, M., Kyrpides, N. and Overbeek, R. Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586
J. Bacteriol. 184 (7), 2005-2018 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T., Lykidis, A., Bhattacharayya, A., Bartman, A., Gardner, W., Grechkin, G., Zhu, L., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A., Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-FEB-2002) Integrated Genomics, Drive, Chicago, IL 60612, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusobacterium nucleatum subsp. 197 of the complete genome. AE016607 AE009951
AE010607.1 GI:19714578
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Fusobacterium nucleatum subsp. nucleatum ATCC 25586
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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/transl_table=11

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2719 AAAATAGAAAACACTTAGAAAAAT 2742
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KKNSNIEGKVEYHINLPI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                    Submitted (07-AUG-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA On Aug 7, 2002 this sequence version replaced gi:18958664.
                                                                                                                                                                                                                                                                                                                         Submitted (27-FEB-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 184509)
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AC113237.2 GI:22128672
AC113237.2 GI:22128672
DRAFT
                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                     Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 184509)
Contact: nisc zoo@nhgri.nih.gov
------ Project Information
Center project name: avx
Center clone name: 070J12
                                                                                                                        Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                               Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  familiaris clone RP81-70J12,
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 184204 bases at least Q40
Consensus quality: 184261 bases at least Q30
Consensus quality: 184294 bases at least Q20
Insert size: 162000; agarose-fp
Insert size: 164309; sum-of-contigs
Quality coverage: 10.51x in Q20 bases; sum-of-contigs
Quality coverage: 9.24x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes

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ACCESSION
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brynt, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavacos, I., Ceasear, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checkand, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus clone CH230-176E2, WORKING DRAFT SEQUENCE.
AC098210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 127823; contig of 17823 bp in length 127824 127923; gap of unknown length 147441; contig of 17518 bp in length 147442 147541; gap of unknown length 147542 147542 147542 147542 147542 147542 147542 14754
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clone_end:SP6
vector_side:right"
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129971. .184509
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/db_xref="taxon:9615"
/clone="RP81-70J12"
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                                                                                                    Foster, P.,
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TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

least Q40 least Q30 least Q20

Center: Baylor College of Medicine Center code: BCM

REFERENCE TITLE

JOURNAL AUTHORS

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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladyn, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Khume, J., Idlebird, D., Jackson, A., Jackson, A., Jackson, A., Jackson, A., Jackson, L., Jackson, K., Johnson, B., Johnson, B., Johivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lozanshewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lozanshewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lozanshewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lozanshewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lu, X., Ma, J., Lozanshewa, L., Loulseged, H., Lozado, R.J., Lu, X., Majum, A., Maheshwari, M., Martin, R., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Maheshwari, M., Maheshwari, M., Maheshwari, M., Martin, K., Martin, R., Martinez, E., Maheshwari, M., Morris, S., Minja, E., Montemayor, J., Moore, S., Minja, E., Montemayor, J., Moore, S., Minja, E., Montemayor, J., Moore, S., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Patez, L., Pfannkoch, C., Plopper, F., Onidexter, A., Popovic, D., Primus, E., Pu, L.-L., Plastrin, R., Martin, R., Reigh, R., Reilly, M., Savery, G., Scherer, S., Scott, E., Riggs, F., Riegh, R., Shen, Y., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Shetty, J., Sheartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, Y.-Z., Sorelle, R., Sosa, J., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warght, R., Mu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Marten, R., Waldron, L., Walter, B., Wang, J., Waldron, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiter, S., Smith, H.O., Richt, H.O., Miller, R., 
                            AL Submitted (13.MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23268092.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 212621)
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    Genome Center
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RESULT 15
AC110715/c
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Best Local Similarity
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                                                                                                                  Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Barlen, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Beryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Depper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugen, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Ferneer, C., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Graddy, M., Guerra, W., Guerra, W., Guerra, W., Hasland, W., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, S., Hlakan, S., Hlakks, S., Hame, J., Idbehird, D., Jakkson, A., Hollins, B., Hakks, S., Hame, J., Idbehird, D., Jakkson, A., Hollins, B., Hakkson, A., Hodgeon, A., Hodgeon, A., Hogues, M., Hollins, B., Hakkson, A., Hodgeon, A., Hodgeon, A., Hogues, M., Hollins, B., Hakkson, A., Honderson, N., Hernandez, D., Jakkson, A., Honderson, M., Hollins, B., Hakkson, A., Honderson, A., Hodgeon, A., Honderson, D., Jakkson, A., Honderson, M., Honderson, A., Hogues, M., Hollins, B., Hakkson, A., Honderson, M., Honderson, A., Honderso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           848 AAAATTAGTTTATTTTCTCTTTAT 871
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jlang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaccus
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h
NOTE: This is a 'working draft' sequence. It currently
consists of I contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the finished sequence as soon as it is available and the accession number will be preserved.

1 212621; contig of 212621 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 213753)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 unordered pieces
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/note="clone_boundary
clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .212621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pred. No. 1;
0; Mismatches
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ORIGIN

Matches

FEATURES

REFERENCE AUTHORS

SOURCE KEYWORDS VERSION ACCESSION

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Mangun, B., Martin, K., Martin, R., Martinz, E., Mangun, B., Mapua, P., Martin, K., Martin, R., Martinz, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Morris, S., Munidasa, M., Murphy, M., Nair, L., Markervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Naokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Naokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Revey, K., Regier, M.A., Reigh, R., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shetty, J., Shartsman, S., Shen, H., Shety, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Savery, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Soergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Weil, X., White, F., Warght, D., Waldron, L., Walker, B., Wang, J., Warren, J., Warren, R., Weil, X., White, F., Waillson, R., Willson, R., Weil, X., White, F., Waillson, R., Willson, R., Weil, X., White, F., Waillson, R., Weil, X., White, F., Waillson, R., Weil, X., White, F., Waillson, R., Weil, X., Woon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Dunn, D., Yon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Dunn, D., Yon, V., Weinstock, G. and Gibbs, R.A.
                                                                                   AL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 19, 2002 this sequence version replaced gi:23680201.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome spatials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 213753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Sequencing Consortium.
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Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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    Genome Center

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JOURNAL REFERENCE AUTHORS TITLE

TITLE

JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Center project name: GSTM

Center clone name: CH330-155723

Center clone name: CH330-155723

Center clone name: CH330-155723

Consensus quality: C303043 bases at least Q40

Consensus quality: 204685 bases at least Q20

Consensus quality: 204685 bases at least Q20

Consensus quality: 204685 bases at least Q20

Estimated insert size: 206221; sum-of-contigs estimation Contact: hgsc-help@bcm.tmc.edu Quality coverage: 6x in Q20 bases; sum-of-contigs estimation Center: Baylor Web site: http://www.hgsc.bcm.tmc.edu/ Center code: BCM College of Medicine

^{*} NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This is a 'working draft' sequence. It currently

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Search completed: September 16, 2005, 15:25:37 Job time : 4110 Becs
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Bource
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                                                                                                                                                            Query Match 1.7%; Score 24; DB 2; Length 213753; Best Local Similarity 100.0%; Pred. No. 1; Matches 24; Conservative 0; Mismatches 0; Indels 0
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                                                                              consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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212726
                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_end_extension
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33891..35390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="CH230-155J23"
                                                                                                                                                              0; Gaps
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Minimum |
Maximum |
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1: geneseqn1980s:*
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4: geneseqn2001bs:*
5: geneseqn2001bs:*
6: geneseqn2002bs:*
7: geneseqn2002bs:*
9: geneseqn2003bs:*
11: geneseqn2003bs:*
11: geneseqn2004bs:*
11: geneseqn2004bs:*
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ALIGNMENTS

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XX RESULT 1 M845; male; tissue-preferred; plant tissue; differentiated; Albertsen 30-DEC-1998. AAX07408; AAX07408 standard; DNA; 1394 BP. WPI; 1999-105628/09. 23-JUN-1997; 19-JUN-1998; WO9859061-A1 Zea mays. Zea mays Ms45 male tissue-preferred regulatory region 08-JUN-1999 (PION-) PIONEER HI-BRED INT INC. Š, (first entry) 97US-00880499 Fox TW, 98WO-US012895 Garnaat regulatory region; plant cells;
maize; hybrid seed; fertility; ss. Ã Huffman GA, Kendall ŢŢ,

The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably with the exogenous nucleotide sequence (a male sterility gene, preferably ms45), which encodes a product selected from auxins, rolB and diptheria Ms45), which encodes a product sele-toxin. Hybrid seeds are produced by and infertile plants New nucleic acid encoding a - useful in mediating plant Claim 2; Page 22-23; 39pp; English. Ms45 male tissue-preferred regulatory region fertility, especially hybrid seed production

cross-pollinating

maize

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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The
                                                                                                                                                                                                                                          A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably
                                                                                                                          New nucleic - useful in
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AAH76333 standard; DNA; 1394 ΒP

AAH76333;

29-OCT-2001 (first

Ms45; male tissue; Z. mays Ms45 male tissue-preferred regulatory region regulatory region; transcription; encoding male fertility; DNA.

hybrid

seed;

WO200160997-A2

23-AUG-2001

13-FEB-2001; 2001WO-US004527

15-FEB-2000; 2000US-00504487.

(PION-) PIONEER HI-BRED INT INC

Š Ψ, Garnaat Ğ. Huffman Ō Kendall

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A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant. comprising nucleotide the MS45 gene useful f for for

Page 47; 50pp; English.

RESULT 4
AAH76333
ID AAH76333
ID CAAH76333
I The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MG45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 may preferred regulatory region from mays 0

Sequence 1394 B₽; 411 A. 309 Ç 232 <u>ი</u> 442 ; 0 Ç

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                                          The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays MS45 promoter fragment
                                                                                                                                                                                                                                                                                                                                                   A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
     Sequence 255
                                                                                                                                                                                                                                                                                                Example 5; Fig
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediatring male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the DNA box of a Z. mays M845 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 47; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2001; 2001WO-US004527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z. mays Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH76334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH76334 standard; DNA; 158 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC
                                                                                                                  1261
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                                                                                                CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                               TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT
                                                                                                                                                                                                                                                                                                                158 BP; 41 A; 50 C;
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                                                                           CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 158
                                                                                                                                                     TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue-preferred regulatory region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TW,
                                                                                                                                                                                                                            8.0%; Sur
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnaat
                                                                                                                                                                                                                                                   Score 111; DB 5; 1; Pred. No. 1.3e-42;
                                                                                                                                                                                                                                                                                                                21 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š.
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                46 T;
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                                                                                                                                                                                                                                                                                                                Other;
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AAH76337
ID AAH7
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Best Local
                                                                                                                                                                         Z. mays M845 male tissue-preferred regulatory region fragment
                                                                                                              Ms45; male tissue;
hybrid seed; ds.
                                                                                                                                                                                                                29-OCT-2001
                                                                                                                                                                                                                                                         AAH76337;
                                                                                                                                                                                                                                                                                              AAH76337 standard;
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                                  WO200160997-A2
                                                                         Zea mays.
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -111 bases upstream of the plant and the plant are present sequence represents a DNA fragment -72 to -111 bases upstream of the plant and plant where the present sequence represents a DNA fragment -72 to -111 bases upstream of the plant and plant are presented regulatory region that the plant and plant where the exogenous gene are presented to plant where the exogenous gene are plant and plant where the exogenous gene are plant and plant where the exogenous gene are plant and plant are plant and plant are plant and plant are pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 BP; 18 A; 17 C;

    mays Ms45 male tissue-preferred regulatory region fragment.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH76336 standard; DNA; 50
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                                                     1229 CTGAACCAAGAGGATACCTACTCCCCAAACAATCCATCCTTACTCATGCAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Page 47; 50pp;
                                                                                                                                                                                                                                                          Similarity
CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCCATGCAAC
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
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                                                                                                                                                                                                                                                                                                          3.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                         5 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                    Score 50;
Pred. No.
                                                                                                                                                                                               Mismatches
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. 2.6e-13;
                                                                                                                                                                                                                                                                                               Length
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regulatory region; transcription; male fertility;

DNA;

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RESULT 9
AAH76335
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediatring male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment upstream of the TATA box of a 2. mays M845 male-tissue preferred regulatory region nucleotide sequence
          Claim
                                A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                                                                                                                                                                                                                     23-AUG-2001
                                                                                                                                                                                                                                               WO200160997-A2
                                                                                                                                                                                                                                                                                               hybrid seed;
                                                                                                                                                                                                                                                                                                           M945; male tissue;

    mays Ms45 male tissue-preferred regulatory region fragment.

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                                                                                                                                                                                                                                                                                                                                                                                          AAH76335;
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                                                                                                                                                                                           13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                      Zea mays
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                                                                                                                                        PIONEER HI-BRED
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          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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          47; 50pp;
                                                                                                              FOX TW,
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                                                                                                                                                                                                                                                                                                          regulatory
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          English
                                                                                                                Garnaat CW,
                                                                                                                                         INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                           region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                Huffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising nucleotide sequences the MS45 gene useful for
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RESULT 10
ABL40437/c
ID ABL404
XX ABL404
XX Sunflo
XX WO2002
XX WO2002
XX Sunflo
PT TATA_8
FT CAAT_8
FT TATA_8
FT TA
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Best Local
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The invention relates to sclerotina-inducible genes and promoters of initiating transcription from sunflower. The polynucleotides are useful for genetically manipulating plants to enhance disease resi or resistance to insect, fungal pathogens, viruses or nematodes. To nucleotide sequences are also useful as genetic markers in disease resistance breeding programs. The polynucleotides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -152 to -181 bases upstream of the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                         manipulating plants to enhance disease resistance or resistance to pathogen, and for producing proteins for controlling plant diseases caused by these pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sunflower; chitinase; lipid transfer protein; LTP; transcription; sclerotina; genetic engineering; disease resistance; insecticide; antifungal; viricide; nematocide; antimicrobial; antibacterial;
                                                                                                                                                                                                                                                                                                                                           New genes and promoters from Helianthus annuus, for genetically
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bao Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-AUG-2000;
07-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-269194/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1179 CATGCTTGTTCAACCGTTTCGTCTTGTTCCA 1208
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                                                                                                                                                                                                       1; Fig 4; 89pp; English.
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2001US-00923844.
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807. .811
/*tag= b
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100.0%; Pr
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Pred. No.
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Best Local :
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producing proteins useful in compositions. The compositions are useful reducing or eliminating damage to plants caused by plant pathogens. The compositions find use in agricultural and pharmaceutical compositions as antifungal and antimicrobial agent. For agricultural purposes, the compositions may be used in sprays for control of plant disease. As pharmaceutical compositions, the agents are useful as antibacterial and antimicrobial treatments. The present sequence represents the promoter
                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer.
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  also useful
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Pred. No.
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RESULT 13 AAI38581/c ID AAI38581

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Best Local S
Matches 21
                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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26-MAY-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                        AAAGGGAGAGAGAGAGAAGA 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACAAAAACTTCCACGGGT 113
AAAGGAGAGAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTACAAAAACTTCCACGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312P.
2000US-0207456P.
2000US-0060840B.
2000US-00632366.
2000US-0234687P.
2000US-0234359P.
2000US-0024263.
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                           IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       liver; gene expression; single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                   86 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                      7172; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 69 C;
                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                   149 C; 70 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
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                                                                                                    Score 21;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 G;
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid probe #7172
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                        No.
                                                                                                                                                                   154 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뮸
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                   0 U;
                                                                                                                          4;
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                                                                                                                      Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 333;
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                                                                                                                                                                     0 Other;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid probe; ss.
                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
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RESULT 14
AAK32768/c
ID AAK32768 standard; DNA; 459 BE
XX
AC AAK32768;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed si
XX
KW Human; bone marrow expressed c
KW microarray; cancer; leukaemia;
XX
OS Homo sapiens.
XX
PN W0200157276-A2.
XX
PD 09-AUG-2001.
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Best Local S
Matches 21
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                          Sequence 459 BP; 86 A; 149 C; 70 G; 154 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                       Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 7267; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI38581;
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                                                                                                                                                                                                                                                                                              1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n genome-derived single exon nucleic acid probes useful for analyzing expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG
                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-488897/53
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                     AAAGGGAGAGAGAGAGAAGA 1057
                                                                                                                                                                                                                                                                        AAAGGGAGAGAGAGGAAGA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.
                                                                                                                             expressed single exon
                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                 1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression
                                                                                                                                                                                                                                                                                                                                     Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                              probe
                                                                                                                                                                                                                                                                                                                                     DB
21;
                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in human placenta sample
                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                 Length 459;
                                                                                                                                ID NO:
                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 15
AAK07027/c
ID AAK07027 standard;
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Best Local S
Matches 21
                                                   04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
         Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                           30-JAN-2001; 2001WO-US000667
                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                     WO200157275-A2
                                                                                                                                                                                                                                            Human; brain expressed exon; g
Alzheimer's disease; multiple
                                                                                                                                                                                                                                                                            Human brain expressed single exon
                                                                                                                                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                                                                                                         AAK07027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 459 BP; 86 A; 149 C; 70 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as lymphoma, leukaemia
the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4;
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53.
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                               (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                          1037 AAAGGGAGAGAGAGGAAGA 1057
         SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for analyzing
expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG
                                                                                                                                                                                                                                                                                                                                                                                                      118
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                      AAAGGGAGAGAGAGAAGA 98
         Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7325; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000US-2007456P
2000US-00608408
2000US-00632366
2000US-0234687P
2000US-0236359P
2000US-00024263.
                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%;
         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                               459
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                               ₽P
                                                                                                                                                                                                                                            gene expression analysis; probe; microarray;
e sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21;
Pred. No.
         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                             probe SEQ ID NO:
         DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         . DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                               7018
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Search completed: September 16, 2005, 13:08:39 Job time: 584.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which are derived from genee expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in \ensuremath{\mathsf{human}} brains.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 459 BP; 86 A; 149 C; 70 G; 154 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 7018; 650pp + Sequence Listing; English.
                                                                                                                                                                  1037 AAAGGGAGAGAGAGAGAGA 1057
                                                                                                                                118
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                                                                                                                                                                                                                                                      0; Indels
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Run on:

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Match Length
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Gapop 60.0 , Gapext 60.0
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1394
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1.5 50263
1.4 601
1.4 2523
1.4 2523
1.4 65459
1.4 374159
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US-09-949-016-15250
US-09-949-016-12426
US-09-949-016-17933
US-09-949-016-17933
US-09-949-016-11823
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US-09-949-016-71
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Sequence 13563, A
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Sequence 15868, A
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Sequence 11824, A
Sequence 145344,
Sequence 10, Appl
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Sequence 11, Appl
Sequence 18, Appl
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Sequence 98, Appl
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                   Matches 1394;
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US-09-949-016-17127	US-09-949-016-12936	US-09-949-016-11755	US-09-949-016-15845	US-09-949-016-13029	US-09-949-016-17258	US-09-949-016-12126	US-09-949-016-16143	US-09-949-016-11813	PCT-US94-04496-25	US-08-545-860D-25	US-08-320-559-25	PCT-US94-04496-27	US-08-545-860D-27	US-08-320-559-27	5217870-1	5217870-1	US-08-482-073-1
Sequence 17127, A	Sequence 12936, A	Sequence 11755, A	Sequence 15845, A	Sequence 13029, A	Sequence 17258, A	e 12126,	Sequence 16143, A	e 1181	e 25,	e 25,	Sequence 25, Appl	27,	Sequence 27, Appl	Sequence 27, Appl	Patent No. 5217870	5	Sequence 1, Appli

ALIGNMENTS

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/880,499 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 0578 TELEPONMUNICATION INFORMATION: TELEPAX: (515) 248-4800 TELEFAX: (515) 248-4844 INFORMATION OR SEQ ID NO: 1: SPONTENCE CHARACTERISTICS: Sequence 1, Application US/08880499 Patent No. 6037523 GENERAL INFORMATION: APPLICANT: Albertson, Marc C. APPLICANT: Fox, Tim W. APPLICANT: Fox, Tim W. APPLICANT: Garl, Garnaat W. APPLICANT: Huffman, Gary A. APPLICANT: Kendall, Timmy L. TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AND METHOD OF USING SAME SEQUENCE CHARACTERISTICS: LENGTH: 1394 base pair CORRESPONDENCE ADDRESS: ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. MOLECULE TYPE: NUMBER OF SEQUENCES: STREET: Darwin Bu: STREET: Box 1000 CITY: Johnston STATE: Iowa LENGTH: 1394 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear COUNTRY: USA linear PE: DNA (genomic) 100.0%; Score 1394; 100.0%; Pred. No. 0; DB 3; Length 1394;

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                                                             TTCTCTAGATTAGTAAAAAGGGAGAGAGAGGAAGAAATCAGTTTTAAGTCATTGTCCC
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TOPOLOGY: linear;
MOLECULE TYPE: DNA
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                                                                                                                                           APPLICATION NUMBER: US/08/880,49
FILING DATE: CONCURRENTLY HEREMY
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STEANNERWES: 6151
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Query Match 94.0%; Score 1311; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1311; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Darwin Building, 7100 N.W.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIN DATA;
CURRENT APPLICATION DATA;
CURRENT APPLICATION DATA;
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APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PIONEER
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                                                                                                                             single
                                                                                             DNA (genomic)
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELLING DATE: 2000-10-20
PRIOR PELLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
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PRIOR FILLING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
PRIOR OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.
SEQ ID NO 13563
PRIOR MANUAL PRIOR PR
Sequence 124441, Application US/09949016

PATENT NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PRILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 124481

LENGTH: 601
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US-09-949-016-13563
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND

FILE REFERENCE: CLOO1307

CURRENT APPLICATION UNMERS: US/09/949,016

CURRENT FILING DATE: 2000-04-14
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US-09-949-016-124481
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PRILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local Similarity
Matches 20; Conser
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity
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SEQ ID NO 147075
LENGTH: 601
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                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/410,784A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                           APPLICANT: MYERS, ALAN M.
APPLICANT: JAMES, MARTHA G.
TITLE OF INVENTION: ISOLATION OF SU1, A
TITLE OF INVENTION: ENZYME, THE PRODUCT
TITLE OF INVENTION: SUGARY 1
                                                                                                                                                        COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                        CITY: Boston
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Pred. No.
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RESULT 8
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15250 LENGTH: 21679
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
                                                                                                                                Matches
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REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: 15U-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
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APPLICATION NUMBER:
FILING DATE:
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                                                        4880 GATTTTTCTTTTCATTCTT 4899
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100.0%; Pred. No. 14;
/ative 0; Mismatches
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Pred. No.
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US-09-949-016-12426/c

Sequence 12426, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

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RESULT 10
US-09-949-016-17933/c
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
Sequence 17933, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                        Best
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SOFTWARE: FRBESEQ for Windows Version 4.0
SEQ ID NO 15868
LENGTH: 374159
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Best Local Similarity
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SEQ ID NO 12426
LENGTH: 65424
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-09-949-016-15868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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LOCATION: (1)...(65424)
OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                               Y Match 1.4%; Score 20; DB 4; Length 374159;
Local Similarity 100.0%; Pred. No. 14;
hes 20; Conservative 0; Mismatches 0; Indels 0
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                       Sequence 41823, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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RIOR APPLICATION NUMBER: 60/241,755
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 601
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for Windows Version
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100.0%; Pred. No.
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100.0%; Pred. No.
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Sequence 145344, Application US/09949016

PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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US-09-949-016-41824/c
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US-09-949-016-41823
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 41823
LENGTH: 601
TYPE: """
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 41824
LENGTH: 601
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ORGANISM: Human
-09-949-016-41824
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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100.0%; Pred. No. 42
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OF DETECTION AND USES THEREOF
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Search completed: September 16, 2005, 08:14:15 Job time : 179.5 secs

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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-145345
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; ORGANISM: Human
US-09-949-016-145344
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 145345
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SOFTWARE: FastSEQ for Window
SEQ ID NO 145344
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
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                                  1038 AAGGGAGAGAGAAGGAAG 1056
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553 AAGGGAGAGAGAGGAAG 535
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100.0%; Pred. No.
                                                                      1.4%; Score 19; DB
100.0%; Pred. No. 42
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                               Score
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seq length: 2000000000
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1: /cgn2 6/ptcdatta/1/pubpna/USO7 PUBCOMB.seq:*

2: /cgn2 6/ptcdatta/1/pubpna/USO6 NEW PUB.seq:*

3: /cgn2 6/ptcdatta/1/pubpna/USO6 NEW PUB.seq:*

4: /cgn2 6/ptcdatta/1/pubpna/USO6 PUBCOMB.seq:*

5: /cgn2 6/ptcdatta/1/pubpna/USO7 NEW PUB.seq:*

6: /cgn2 6/ptcdatta/1/pubpna/USO8 NEW PUB.seq:*

7: /cgn2 6/ptcdatta/1/pubpna/USO8 NEW PUB.seq:*

8: /cgn2 6/ptcdatta/1/pubpna/USO8 NEW PUB.seq:*

8: /cgn2 6/ptcdatta/1/pubpna/USO8 NEW PUB.seq:*
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Gapop_60.0 , Gapext 60.0
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ALIGNMENTS

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Sequence 1, Application US/10713381

| Sequence 1, Application No. US2004022131A1
| Publication No. US2004022131A1
| GENERAL INFORMATION:
| APPLICANT: ALBERTSEN, MARC C.
| APPLICANT: FOX, TIMOTHY W.
| APPLICANT: HUFFWAN, GARY A.
| APPLICANT A.
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Best Local Similarity
Matches 1311; Conserv
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARY
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR PILING DATE: 1997-06-23
NUMBER: OR SEC ID. NOS. 24
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                                              TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT
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RESULT 3 US-10-713-381-9

Sequence 9, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:

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Sequence 3, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: HOFFMAN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: KENDALL, TIMMY L.
FITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/80,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PRICENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ALBERTSEN, MARC C.

APPLICANT: POX, TIMOTHY W.

APPLICANT: GARNAAT, CARL W.

APPLICANT: HUPFMAN, GARY

ITILE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME

FILE REFERENCE: 578R

CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT APPLICATION NUMBER: 08/80,499

PRIOR APPLICATION NUMBER: 08/80,499

PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NO 9

SEQ ID NO 9

LENGTH: 255

TUDE: NAME

LENGTH: 255
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US-10-713-381-3
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Best Local Similarity 100.0%;
Matches 157; Conservative
                                                                                                                                               Matches 111;
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                                                                                                                                  Local Similarity
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                                                                                         TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260
                     CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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                                                                                                                                                 Conservative
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b; Pred. No. 6.9e-45;
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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
CRGANISN: Zea may8
; Sequence 6, Application US/10713381
; Publication No. US20040221331A1
                                      US-10-713-381-6
                                                                RESULT 7
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Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNANT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
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Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)B

FULE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 1857

LENGTH: 1663
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Best Local S
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Best Local Similarity 100.0%;
Matches 70; Conservative
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ORGANISM: Zea mays
FEATURE:
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                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                   1229 CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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Pred. No.
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FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 30
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-4
                                                                                       RESULT 9
US-09-32-844B-5/c
US-09-923-844B-5/c
; Sequence 5, Application US/09923844B
; Patent No. US20020166143A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CORL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.2%; Score 30; DB 20; Best Local Similarity 100.0%; Pred. No. 0.00039; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10713381 Publication No. US20040221331A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.9%; Score 40; DB Best Local Similarity 100.0%; Pred. No. 3.0 Matches 40; Conservative 0; Mismatches
APPLICANT: Pioneer Hi-Bred International, Inc. APPLICANT: Bao, Zhongmeng APPLICANT: Lu, Guihua TITLE OF INVENTION: Sclerotinia-inducible Genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARY
APPLICANT: HUFFWAN, GARY
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 40
TYPE: DNA
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Sequence 56524, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel: Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: WRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION UNMBER: 09/785,276

PRIOR FILING DATE: 2003-02-16
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; ORGANISM: Hellanthus annuus
US-09-923-844B-5
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Publication No. US20030232334A1

GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: 529452000121

CURRENT APPLICATION NUMBER: US/10/085,117

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 361
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SEQ ID NO 5
LENGTH: 849
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CURRENT APPLICATION NUMBER: US/09/923,844B
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/224,603
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: variation
LOCATION: (1)...(194945)
OTHER INFORMATION: n = any nucleotide
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23; Conservative
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Similarity 0; Mismatches
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Pred. No. 1.7;
                                                                                                                     COMPOSITIONS, KITS, AND METION. ASSESSMENT, PREVENTION,
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 183040
LENGTH: 356
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; OTHER INFORMATION: Clone ID: MRT4577_98517C.1
US-10-425-115-183040
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US-10-425-115-117183/c
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                                                                                                     Sequence 117183, Application US Publication No. US20040214272A1 GENERAL INFORMATION:
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LENGTH: 333
                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
                                                                   APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 2000-02-17
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                                                                                                                                                                                                                                                          632 TTTTTCTTTTTCATTCTTGTT 652
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                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                             Application US/10425115
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; Pred. No.
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RESULT 14
US-09-864-761-11465/c
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 117183
LENGTH: 386
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                         PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                    APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00664
PILING DATE: 2001-01-30
                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00666
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Sequence Listing
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Search completed: September 16, 2005, 12:49:09 Job time : 1294.5 secs

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; OTHER INFORMATION: Clone ID:
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; Sequence 51470, Application US/10425115
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 51470
LENGTH: 1203
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Best Local
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
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NAME/KEY: unsure
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ORGANISM: Zea mays
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INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64
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CG224225 OGMDQ20TV
CC656939 OGMDQ20TV
CC6224211 OG1AG08TH
B2828689 PUFHM74TB
B2828689 PUFHM74TB
B2828694 PUFHM74TD
CG1148339 PUKBG46TB
CG011564 ZUART23TV
B2371637 ie38h03.b
CC810403 ZMMBBc047
CG305519 OG0GM20TV
CG190609 PUIHB82TB
CG190609 PUIHB82TB
CG190609 PUIHB82TD
CC358144 PUHPY12TD
CG397825 OGWBG01TH
CC013382 PUFWB51TD
CC439146 PUFWB51TD
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ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CC656933 LOCUS 8 뭉 ORIGIN FEATURES COMMENT DEFINITION Query Match Best Local Sim Matches 910; TITLE JOURNAL source 404 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATTAACC 463 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 963) 1 (bases 1 to 963) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Zea mays Zea mays CC656933 OGWDQ20TM ZM_0.7_1.5_KB genomic survey sequence. CC656933 Unpublished (2002) Other_GSSs: OGWDQ20TV Class: sheared ends. Seq primer: TR Email: whitelaw@tigr.org Tel: 301-838-5843 Fax: 301-838-0208 9712 Medical Center Drive, CC656933.1 Similarity Contact: Cathy Whitelaw Conservative 1. .963 /organism="Zea mays" /mol_type="genomic DNA" /clone="ZMMBMa0554D15" /clone_lib="ZM_0.7_1.5_KB" /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 methylation filtered genomic_DNA library" Location/Qualifiers /strain="B73" /db_xref="taxon:4577" GI:32060225 100.0%; 65.3%; ; Score 910; DB %; Pred. No. 0; 0; Mismatches Zea mays Rockville, đq DNA linear GSS 19-JU genomic clone ZMMBMa0554D15, B 9; 3 <u>.</u> Length 963 20850, USA Indels GSS 19-JUN-2003 ٥, õ Gaps 60 0

ck, T., Rohlfing,

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Best Local Similarity
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E 1 (bases 1 to 915)
S Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlf Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
L Unpublished (2002)
Conter GSSs: OG1AG08TH
Contact: Cathy Whitelaw
TIGR Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Class: sheared ends.
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                TGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATA
                                TGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATA
                                                                    ATAGGTGCCTACGTCAGGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCT
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/mol type="genomic DNA"
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methylation filtered genomic DNA library"
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1. .915
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%; Pred. No. 0;
0; Mismatches
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RESULT 3
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1 (bases 1 to 687)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)
Other_GSSs: OGWDQ20TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC656939 687 bp DNA line CGWDQ20TV ZM 0.7 1.5 KB Zea mays genomic clone genomic survey sequence. CC656939 CC656939.1 GI:32060231 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                      Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-5843
Fax: 301-838-0208
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              AGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCAGG
                                                                 CTCTAGATTAGTAAAAAGGGAGAGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCCTG
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/clone=1ib="ZM 0.7_1.5KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Pred. No. 1.2e-237;
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                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
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genomic survey sequence.
CG224211
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1324 GATCACAACAGCTAGCGTTCTCCCGCTAGCTTCCCCTCTCTCCTCTGCCGATCTTTTTCGT
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Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGIAGOSTV
Contact: Cathy Whitelaw
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1 (Dases 1 to 878)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
AGATCACAACAGCTAGCGTTCTCCCGCTAGCTTCCCTCTCTCCTCCGATCTTTTCG
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/mol_type="genomic DNA'
/strain="B73"
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/clone="Ibb="ZM 0.7_1.5KB"
/note="Vector: pBCSK:, Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                               Score 66; DB 9; L
Pred. No. 5.4e-22;
0; Mismatches 0;
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Matches 27; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 611)
Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                             Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUFHM74TB
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1 (Dases 1 to 539)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
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GSS.
                                                                                              Bennetzen, J.
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BZ828694
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PUFHM74TD ZM_0.6_1.0_KB Zea r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennetzen, J
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Medical Center Drive, Rockville,
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Conservative (
                              Cathy Whitelaw
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/strain="B73"
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Best Local Similarity
Matches 27; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 804)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
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GSS.
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PUKBG46TB ZM 0.6_1.0 KB
genomic survey sequence.
CG148339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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Location/Qualifiers
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Class: sheared
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
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TTTTTCAAAAAAATTAGTTTATTTT 182
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                   TTTTTTCAAAAAAAATTAGTTTATTTT 863
                                                         1.9%; Scilarity 100.0%; I Conservative 0;
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/clone="zMMBTA0780G19"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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/clone=lib="ZM_0.6_1.0_KB"
/clone="Vector: pCR4-1.0FO; Site_1: EcoRI; 0.6-1.0 kb high
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/strain="B73"
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tive 0; Mismatches
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Pred. No. 0.052;
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Matches
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CG011564.1 GI:
GSS.
Zea mays
                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 687)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                      Zea mays
Zea mays
                                                                                                                                                                                                                                                                              BZ371637

687 bp DNA linear GSS 26-NOV-2002 ie38h03.bl WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone ie38h03.5', genomic survey sequence.

BZ371637

BZ371637.1 GI:25455537

GSS.
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1 (bases 1 to 854)

1 (bases 1 to 854)

1 (bases 1, Cousckenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
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Other_GSSs: ZUABT23TH
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Fax: 301-838-0208
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ZUABT23TV ZM_3.0_4.0_KB Zea mays genomic clone ZMMBPa0018C22,
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Annenberg Hazen Genome Sequencing Center Spring Harbor Laboratory
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/mol_type="genomic DNA"
/strain="B73"
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/clone=11b="ZM 3.0_4.0_KB"
/note="Vector; pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
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100.0%; Pr/
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Pred. No. 0.17;
0; Mismatches
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Zea mays
                                                                                                                                                                                                               190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                     Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C. Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mccombie@cshl.org
Plate: ie38 row: h colun
Seq primer: -21M13UnivFwd
Class: shotgun
                                                                                                                                                       Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                       Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                    Unpublished (2003)
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Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                          Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                          University
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Location/Qualifiers
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                                       /mol_type="genomic DNA"
/cultivar="B73"
                                                                       organism="Zea mays"
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/clone="ZMMBBc0479C04"
                    db_xref="taxon:4577"
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/cultivar="B73"
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CG305519
CG305519 GI:34219733
GSS.
                                  CG190606 825 bp
PUHPB2TB ZM 0.6 1.0 KB Zea mays
genomic survey sequence.
CG190606
CG190606.1 GI:34081667
GSS.
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25; Conserv
            Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                       Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-5843
Fax: 301-838-0208
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Other_GSSs: OGOGM20TH
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/clone_lib="ZM_0.7_1.5_KB"
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methylation filtered genomic DNA library"
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/strain="B73"
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Zea mays
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Whitelaw, C.A., Quackenbush, J.,
Resnick, A., Fraser, C.M., Yuan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence CG190609
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1 (bases 1 to 825)

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                                                                                                                                                                                                                                               Unpublished (2003)
Other_GSSs: PUIHP82TB
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PUIHP82TD ZM_0.6_1.0_KB
                                                                                                                                              Email: whitelaw@tigr.org
                                                                                                                                                                 Tel: 301-838-5843
Fax: 301-838-0208
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/mol_type="genomic DNA"
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/clone=1betor: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
/note="Vector' pCR4-TOPO; Site_1" CORI; 0.6-1.0 kb high
COT selected genomic DNA library"
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l,P., Ma,J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Whitelaw
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Search completed: September 16, 2005, 17:48:56 Job time : 4301.5 secs
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1 (bases 1 to 878)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: GGWBGGITV

Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: TR
Class: sheared ends.
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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31 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTTGCTCAT	21 CTCCATGTTGCACGTTCCCCACCTTGCACATTTGCACATTTTCTTGGATTGGTCGGTTGGTT	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	Query Match 100.0%; Score 1394; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 3.7e-270; Matches 1394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577"	11394	Location/Qualifiers	Patent: WO 0160997-A 1 23-AUG-2001; Patent: WO 0160997-A 1 23-AUG-2001; Patent: HI-RREN INTERNATIONAL INC (IIS)	Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.		<pre>guraryvra; viriuipianide; sreprophyva; mmuryophyva; iacheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.</pre>	Zea mays	Zea mays		AX224394.1 GI:15554636	AX224394	. h	

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                                                                                    GGTTCGGCAGCTCTCGTGTCATCTCACATGCCATACCATGCTTGTTCCAACCGTTCGTC
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	QY 1321 AAAGATCACAACAGCTAGGGTTCTCTCCCGGCTAGCTTCCCTCTCTCT
	Db 1321 AAAGATCACAACAGCTAGCGTTCTCCCGCTAGCTTCCCCTCTCTCCCGCCGATCTTTT 1380
	Qy 1381 CGTCCACCATG 1394
	Db 1381 CGTCCACCATG 1394
	RESULT 2 BD062176 LOCUS BD062176 1394 bp DRETNITTON Male tissue-preferred regulatory region and method of using same.
	ION BD062176 N BD062176.1 GI:22607781 DS JP 2001520523-A/1.
	Homo sapiens (human) SM Homo sapiens
	REFERENCE 1 (bases 1 to 1394) AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall T.
	TITLE Male tissue-preferred regulatory region and method of using same JOURNAL Patent: JP 2001520523-A 1 30-OCT-2001;
	COMMENT PN JP 2001520523-A/1 PD 30-CCT-2001
	PF 19-JUN-1998 JP 1999504910 PR 23-JUN-1997 US 08/880499 PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
· · · ·	PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC,C07K14/34,C12Q1/68,
	PC A01H5/00 CC Strandedness: Single; CC Topology: Linear;
	FEATURES FEATURES Location/Qualifiers Source 11394
	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
	Query Match 100.0%; Score 1394; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 3.7e-270; Matches 1394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	QY 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60
	QY 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCCACGGGTGCATGAT 120
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	QY 121 CTCCATGTTCCACCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTTGCCCAT 180
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	OY 241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGGATATATGTCCCCCACAATCGTCACCTATA 300
	241 CGAGACGIAICGGGIGGIGAICCAGGGGAIAIAIGICCCCCACAAICGICACCIAIA
	Db 301 TTATTATTCTTTAGATATTTATTTTAGAAAAATTAACAAACTTATACTTTTGTGTA 360

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Submitted (13-MAR-2001) Trait and Technol
Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave.,
IA 50131-1004, USA
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Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3343)
Fox,T.W., Trimnell,M.R. and Albertsen,M.C.
Cloning of Ms45, a gene required for male
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Fox, T.W., Trimnell, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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join(<1392 ... 1768,1898 ... 2182,2280.
/gene="M845"
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d Ave., P.O. Box 1004, Johnston,
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                                  CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACCACGATCCTCTTAAAAAACCACGATCCTCTTAAAAAACCAAGATCCTCTTAAAAAAACCAACGATCCTCTTAAAAAAACCAAGATCCTCTTAAAAAAACCAACGATCCTCTTAAAAAAA
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/mol_type="unassigned
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and
Kendall,T.L.
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/mol_type="genomic DNA"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                   Albertsen, M.C., Fox, T.W., Garnaat, C.W., Male tissue-preferred regulatory region Patent: WO 016097-A 9 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US)
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REFERENCE
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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RS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Cooke, R., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., McLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Mayen, T., Nicol, R., Norbu, C., O'Connor, T., Naylor, J., Nguyen, C., Ngyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stoubs, M., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Choepel, Y., Collymore, A., Cook, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karates, A., Kells, C., Landers, T., Levine, R., Unchella, C., Karates, A., Kells, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., MacConnald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacGonald, P., Major, J., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Neuton, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peteron, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 17, 2004 this sequence on replaced gi:49658659. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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mays, clone ZMMBBc0334A01
                                                                                                                                                                               Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                         Center code: WIBR
                                                                                                                                                                                                                                                                                                                 ------- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Matches 115;
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162177 TTTCCAAACTAACCCTCAAGTATATAATGAATGCAGGACAA 162217
                                                                                                                           162117 TTCTAAGTGAAATTAGTTCATTTTCTCTTAACAAATAGAAATTTATTGGTAAAATAGAG 162176
                                                                                                                                                                                                                                                       162058 CTTTTCTTTTACTTTTAGGGCTAGTTTGGGAÄCCCTATTT-TTCTAAGAÄATTTTCÄTTT 162116
                                                            900 TTGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAA 940
                                                                                                                                                                840 TTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGAG 899
                                                                                                                                                                                                                                                                                         This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This casembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nnih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at
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Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * consists of 6 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have * provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.broad.mit.edu/annotation/plants/maize/randomclones.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available and the accession number will be preserved.

1 100617: contig of 100617 bp in length 100618 100717: gap of unknown length 100718 104730: contig of 4013 bp in length 104731 104830: gap of unknown length 104831 115104: contig of 10274 bp in length 115105 115204: gap of unknown length 115205 156396: contig of 41192 bp in length 115205 156396: contig of 41192 bp in length
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100718
104731
104831
115105
115205
1156397
156497
179937
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Center clone name: 334_A_1
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
/clone="ZMMBBc0334A01"
/clone_lib="CHORI-201 Maize B73 BAC MboI Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .186199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186199: contig of 6163 bp in length
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179936: contig of 23440 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                 5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180036: gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 186199;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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DEFINITION

AC117267 25769 bp DNA linear INV 21-FEB-20 Dictyostelium discoideum chromosome 2 map 5836255-5862024 strain AX4, complete sequence.

INV 21-FEB-2004

CDS

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REFERENCE
AUTHORS
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ORGANISM
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JOURNAL
MEDLINE
PUBMED
REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Feb 21, 2004 this sequence version replaced gi:19570016, gi:20087114.

CDS predictions from GeneID may contain errors. Further Information
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 25769)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 25769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence and analysis of chromosome 2 of Dictyostelium discoideum Nature 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noegel, A.A.
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AC117267.2 GI:42733680
                                                                                                        /translation="MEFPTKYVYITSNLDKPKEWFTQSEMSLITTTDTIQKSFVNNSG
SSSSSKGFGEAVLLDILDTAGQEEYSAWRDQYVRTGDCFMIVFSIDSRSSFEEVSQLK
QHIERVKDRDDVPIITGMKVDLESRRQVSRIEBADQLARSLRVPYIETSAKTRSNIES
AFFTLVRHTPRNTVYKVVMGGGGVGKSAIIIQFIQHTVEEYDDTIEBSYRKQVTIS
GLPPIGGSLNKKSSSSSSSSSSSSKTCLFNKIFSGKDKQPSPQQAASBSTIDRTGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deutsche Forschungsgemeinschaft (DFG) Location/Qualifiers
                           STURLEANVLSYSMSNLSKEVPLITGDCVYCQGCNVILSRFSNLVKTGDDSFTWKCEF
CKYSNSNILLEQGEIPNKDSVEYVLSSPSTSSTTDGSKREESIIIYCIDVSGSMGITT
EVPSLQSEWVNAKKGVKGASSGPSYISRLECVQSSIPTMIDRLSIQYPNKRVVLVTFS
                                                                                                                                                                                                                                                                                                                                                                              /note="GeneID exon scores (in ord 24.88, 254.96 - GSCJ_ID dd_00753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="WRLQIILFLSILLIFQLKSTFSSNDISSTILSITPNFNKDYNNQ
ILSKSEWFRSLEYSSNKKVIFBVFDGFRHEYIENLDRIIKEREKKYYGVDFSFSSCL
NSKENYLEVLKKFSTISRNNKYYBFBIJWHUIESTHENCYNUSNYLYNKKNINEYQBYLV
FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENNKDKLFSSLPFFYLKNIAENQEFEDYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(832. .1070,1237. .1349,1533. .1798,
1896. .2053,2231. .2360))
/note="GeneID exon scores (in order of location ranges):
23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
DEVMIYTQSNSVDGPIVIAGDKLEDFDQLIEIGRSMTYDKLPTASGSSDFLKAKIKSI
                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="AAS38626.1"
/db_xref="GI:42733682"
                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSGSGSSGTSGAQLSGTGYVINHQ"
join(2957. .3173,3272. .5583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSPLGSWTDFKIKQFKKLNDIETILSDVEVNLCSSSNNNNNNNNVDDETLTLLGSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
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/db_xref="GI:42733681"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="AX4"
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                                                                                                                                                                                                                                                                                                                                                                                                               order of location ranges):
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TLANERINGNDGEITTTTTTTTSÄSSTTIMTTTTTNGVNDRNYLLFRQVWRNIVIK
TQILFHIRLYNIHANKKVFLTPIQLVDYKKGYLQSMVINYHDDNDDDADEDS YDSDI
DDDDSYBDGGNCSSSSGSSDIGSSSNSINNGISNSSSSSILSNSSLLELSMIRVNIL
PEGLKSIEFEKEYNVIQDRLLPPSISSIRFSYGFNQRIAKGVISDNVISITFGDSFNQ
SLDGNWLPKQLKHLQFGHKFQQTIKMGQLPSSITSLILDPRSYGVIEIGSIEPGBHFNS
LDYKFNSCSNGVESISFNPIPGEITRLVFDSEFNQNIKANDISSNYNLTSIHFGBHFNS
DIGIKSLPNSIREIKFGRAFDRDIKLCPSSITSIDFGNKFNRPLSMMTQTLTSIDFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="AAS38629.1"
/db_xref="01:42733685"
/translation="MEEKIKFYFEIIDFQNQKFKIQEFTSKLIGLKEESFTTFKPIVY
/translation="MEEKIKFYFEIIDFQNQKFKIQEFLEXEPFIVFLKESFOIL
EKYLKMTQSIESSILKTNGTINKSIFEBFFYCGYIGEFLEXEPFIVFHKESFOIL
DDYIFEKINKLMKLMEKEKLINSLIYYNNKMENKIGFEFMEJINFQGFTHKESFOIL
INANSLMIKSSIDSRNISNSPINSRCSFNEYFEKRSSDASGDFILTISMIGIMDNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPKSNKKINDVNAAFAAVANSTTTTEQPVÄIIDGATPSTNESPKKTPLKETDPKRLAARQRQIDIGKMTAGYKNYIALVPKSKRKPTDPKTPNKNQVCSKRSWDGQIKKWRRQLHENDWTGIPRKEKEVEASNNESTEESTLEKEMNKLEISBENENHNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPVQSTALGPALLVSAAIASQKMLSEVVICTDGVPNVGLGAIEDLPLGPAQEFYEKVT KLAQNIKTINIIGISGSHIDLGVIGKVSEQTMGNIIIIHPLELAREIRKLTQNIPMI TUVBHSICLHPTLEINKYDSKQGLSRVVKQFPNVNSLTDLTLLYSSNIRPTEFVQIY PFQIQIKYTKLLGVRCLRVVSAQLQATEDFNTSTSNANISILAMAFTQQAKIAQQQEY MESRLHLKAATKLIRSLCNTDEQWEEFYNFEVLREEMEAPLITCIKNKQQRVEKAATD
                                      CYGISNKGGFGSNSSSNFCVGGTNNGLREMLKNTTSLKTLTLNYFNRKIEVGDLPNSI
                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdnL1ydfL1kKEYNQQSFLDC1L1LS1NGLY1SYDGLLDYCNN
FRL1ENKTVNKEAISYYGLNYNQYQLLDEFTRLLKLKNKTTDCKNKIINTHNSLNKCC
GNNKFDYSIL1IIENNNNIINKDYQFNNNNKNSNNNIYNNNNDNNNSIIEEKDLNKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="similar to Dictyostelium discoideum (Slime mold). Hypothetical 97.7 kDa protein" (protein id="A8338630.1" /db_xref="GI:42733686"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENSIIESKEFQTINYHAKSFFLLINDLYSFNREINENDLLNYIKILAIQLNSIQLSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="GeneID exon scores (in order of location ranges):
23.29 - GSCJ_ID dd_00728"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTDAFVAASSSSSVKYTIDVLLSFKSANTKRPIQIDIVENHQKEIVVPLSLETTPYN
NNNNNNNTNNSQHNTANGQKYPIFSPQISPFKIAYAQSSSTKTNINNNNNNNITP
TKKANSNITTPQSNNENNHYNSNTKSSTKKQNPIPFSLNTATPNQKNTTTTPSKKSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSSSTIITPIATTTTNNNSSTNGIHNSKTNRTLFKNIKNNIKNSIPNS
PNNAPIKKNSVGIIGNGPNVNNNNKDRKLNSNDGVNFGKKNILFTPSKNSMVSTTKHS
SSSSSLLAKNEYDIESIKKELKSMDISTGGISPLSSPLRESSPISTIDLESITATTTK
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Hypothetical protein"
/protein id="AAS38627.1"
/db_xref="GI:42733683"
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68.61 - GSCJ_ID dd_00752"
ESLNLGYHFNQPIGNNVLPKLLKKLFILNSEFNQNISADGCIPFGLQTIYIRNSNMNF
                                                                        KFNQIIPQGIFIHTKLKSLNFGYHFNQIIPADTLPPTLESLNLGGYNREITVKNDEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(10972. .11979)
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/protein_id="AAS38628.1"
/db_xref="GI:42733684"
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/note="GeneID exon scores (in ord
/no.37, 128.60 - GSCJ_ID dd_00729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5711. .6796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(12884. .13020,13172. .15320)
/note="GeneID exon scores (in order of location
2.42, 136.56 - GSCJ_ID dd_00727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTIELIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNSNKILSGIYFAHKKSKRY
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Best Local Similarity
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TTTCTTCTCTCACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATT
                                                                                ATAAAATATTAATTAATTATTAAA-ATTATTTTCTTATTTTTATTTTAATTGAAAAAT
                                                                                                                                                                                                                                        AGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                        TGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAG 557
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                                                                                                                                                   CTATGACGTTCAGATTTTTCTTTTCATTCTTGTTATTTGTTATTGTTTTTATATACAT
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/product="hypothetical protein"
/product="hypot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSKVYSKSQTVSPGKPQNIFVTALPSSVSAPSLLSLQKPNNGAG
SHKKQRQNSGSSKORPNLFLDQIKSTERKNSGNKSNNNNNKRKKYSKNNSNVNSNNIN
SSSIVIKCEEQQQQQQQQQQQQQQQQQDGFLKSQEFPNLFKNKLYLKDDIS
SPSSSSTSSPSCLSSSSSSTFSQSEIAENKDDINNNCNNTNGNFEEEEEEEKNKV
EQQSIEEETFIESSFEETKEVVEEVPFEEQFEILPISIGEETLKEYTSFLSVLSELIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="similar to Arabidopsis thaliana (Mouse-ear cress). Putative PREG1-like negative regulator" (protein ida-"AAS38633.1" /db_xref="G1:42733689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINPREGGNIYQSIKN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSTIQFNEKLFSLVYIPFYYTKYEFQNQSFSFFLNSQNGVISATRPEIGLGKIGDFLK
YTQNYFSTLVGNFEPFSKCKGDELAIIDSFKVYNTSSYFLTFSRSSTNFLGSSSIGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCVKVHIDRCSLRCPHGHECKVDHNCKECCVRSHRPPPPEVCSLRCPPKHECKPDDHG
KKCCVKIHCDEVCDLDCGRGFECKIRHDECKYCVRSERPHPPGHEKKNRKCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVHFGEECCVXVHIDKGSLRCPPGHEKK
VDQHGKECCVVAHRPPPKCSLRCPPKHECRINHFGEECCVKSRNDCLTCEDLNCERKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCPIGHICVEDSNGVNCVPNGGGTSGGSSSTGTSGGHPDPCRDVDCPDGFHCECKDGK
TAKCVPSPTTGSSSTSGGHPDPCKDVTCPDGFHCECKDGKTAKCVPSPTTGSSSTSGG
NTNPCSNVNCPDGFYCECKDGKTAKCVPSGPTQPPKPPVCSLRCPPNHECRFNDQGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mfIGEDCNKITNEEECHKSSECIVINYTPCCGEQKWACSKGTFD
TCTYENSCYRNSSNNQVVEVSNKCFNLDGFIKITTPTEYSCSDAKIKECALLGKSCSF
QKNSCSNPTSCCPGESICEGLSSGSSTSGGGSSGGTSGGSSSGGTSGGSSSGGTSGSS
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/db_xref-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (21961. .24357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="GeneID exon scores (in order of location ranges):
106_68 - GSCJ_ID dd_00725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(16184. .16199,17272. .17613,17707. .19331)
/note="GeneID exon scores (in order of location 0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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49.4%;
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ln_id="AAS38631.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73.4; DB 3; Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SP87 precursor (PL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25769;
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Dechering, K.J., Kaan, A.M. and Konings, R.N.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria paras Plasmodium falciparum (1. Cell. Biol. 19 (2), 967-978 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 713)
Dechering, K.J., Kaan, A.M., Mbacham, W., Wirth, D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum sexual stage antigen (\mathfrak{s}16) gene, promoter and partial cds. AF034389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-NOV-1997) Molecular Biology, University of Nijmegen,
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Location/Qualifiers
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                                                          Conservative
                                                                                                                                                                                                                                                                        /gene="816"
537. .710
                                                                                                                                                                                                                                                                                                      /gene="816"
537. .>713
                                                                                                                                                /codon_start=1
/product="sexual stage
/protein_id="AAD12581.1
/db_xref="GI:3098291"
                                                                                                                                                                                                                                                                                                                                                 /gene="816"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="NF54"
                                                                                                                                     translation="M"
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                                                                                                                                                                                                                           'gene="816"
                                                                                                                                                                                                                                                         /gene="816"
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                                                                       5.1%;
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                                                         Score 71.2; DB 3;
Pred. No. 0.00041;
0; Mismatches 333;
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                                                                                                                   2 (bases 1 to 3576)
2 (bases 1 to 3576)
Escalante,R., Wessels,D., Soll,D. and Loomis,W.F.
Direct Submission
Submitted (27-JAN-1997) Department of Biology, University of
                                                                                                                                                                                                                Mol. Biol
97453232
                                                                                                                                                                                                                   Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 3576)
Escalante, R., Wessels, D., Soll, D.R. and Loomis, W.F.
Chemotaxis to cAMP and slug migration in Dictyosteli
on migA, a BTB protein
Mol. Biol. Cell 8 (9), 1763-1775 (1997)
                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum MigA (migA) gene, U86962
                                                                                                                                                                                                     9307972
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             /sub_strain="AK244"
/db_xref="taxon:44689"
/chromosome="4"
                                                                                                        Location/Qualifiers
                                                     /etrain="AX4"
                                                                               organism="Dictyostelium"
                                                                                                                                                                                                                                                                                                                                                GI:1841871
                                                                 _type="genomic DNA"
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TATTITGTTATTGTTTATATATACATTTTCTTCTCTCTACAATAGAGTGATTTTCTTCCGA 711
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                                                                 AGCGACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGT 651
                                                                                                                                                                       TAATCCACTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCT
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="essential for slug migration"
/notee"N-terminus of this protein is similar to other BTE
/omain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
U14556 and L16896, respectively"
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                                                                                                                                                                                                                                                                                                                               2998. .>3423
/gene="migA"
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TNGEQWTVLKRHTNDPSLNYKYATHSWPVTGCETAFRYFRILQTGKNSNNRNFLVIGG
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TDIKIKCGGQIFPTHRIILANSSEFFGRLLLSDFKESSQSVIELKQPDPFNVFPMVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster
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/replace="pbsrl external
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/db_xref="GI:1841872"
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Pred. No. 0.00039;
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plasmid, approximately 4
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                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 1100% of reads
Consensus quality: 149526 bases at least Q40
Consensus quality: 149526 bases at least Q30
Consensus quality: 149526 bases at least Q20
Insert size: 149526; sum-of-contigs
Insert size: 149526; sum-of-contigs
Insert size: 149176; 6.5% error; agarose-fp
Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
coverage: 12.54x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:53850295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149526 bp
Danio rerio clone CH211-117K16,
BX957346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC Web site: http:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: zC117K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 149526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beasley,H
                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGATTTTTTCAAAAAAAATTAGTTTATTTTCTCTTTAT 871
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                                                                                                                                                                                                                                                                       the finished sequence as soon as it is accession number will be preserved.
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                                                                                         /note="assembly_fragment:03115
clone_end:SP6
vector_side:right
                                                            vector_side:left"
                                                                                                                                                                         /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-117X16"
                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                               .149526
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5.1%;
46.8%;
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                                                                                                                                                               _11b="CHORI-211"
Score 70.8;
Pred. No. 0
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DB 2;
               Length 149526;
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                                                                                        Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornaby, T., Holroyd, S., Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Kerhornou, A., Knights, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Ratbinowitsch, B., Rajandream, M., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitchead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724 ACTATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTT
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Plasmodium falciparum MAL4P1.
AL034557 AL844503
AL034557.8 GI:23498126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata;
                        Sequence of Nature 419
                                                                             Barrell,B.G.
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                          of Plasmodium falciparum chromosomes 1, 19 (6906), 527-531 (2002)
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Hamilin,N., Pain,A., Berriman,B., Hall,N., Bowman,S., Churcher,C.,
Harris,B., Harris,D., Lawson,D., Quail,M. and Barrell,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambrid
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12368867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKGLDABEAKEI KHLROMLEQAGVRDLAAVGGPCTEGGVAEQNTIMDKFLDEELKEAE CCKNCCKEKAQOEGPCGARSADSPAGTEDHPDAEDDDDDDDDDDDDEDEEEEEED POCKTUNDILGTDDRTKOVEPRROKCLL YVIAHESETKNI ETQDDLRDAFIRTAAAETFLSWQYYKI KNGADAKQLDNGTI PEEFL YYIAHESETKNI ETQDDLRDAFIRTAAAETFLSWQYYKI KNGADAKQLDNGTI PEEFL YRSMYFTYGDYRDI CLNTDI SKTYNNDVAKAKDKI GKFESKLOGSKSSGTTTPODWWQTY GKDI NKGMI CALTHGYTNTEKKTKI KNDYS YDDKVNQSQNGNBSLEDFAKKAQFERWNI ENGGEEFCAERGKLEQNIGKSCNGINFI QYCSDNRHPCNKACDEYKNYVETKQKEFRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRWFEBWAEDPCLIRCHKLKDAIKKCRGKNGEBKYCDLNRYDCKNTASGKHVFFEDFDCKCQYSCAPFVDWIDWCLEFLKQRKKTKEITSGSCGGSGRKKRDATTRYBEYEKKFYKELKGTKKYCVAWIDWCLEKLNDEDVCTKNINDIKDGRIDPKNVHSGSAKKGDGNIKTFYRTKRITSGSKKYVHSGSAKKGDGNIKTTFYRTKYCEACPWCGABKVEGGWKAKEBNCSQTKDYDPKTTTIEILTGDTRKSDMVQKYKKYCKGACPWCGABKVEGGWKAKEBNCSQTKDYDPKTTTIEILTGDTRKSDMVQKYKKFCKGGGRGKGSAFPNATSREKGKKGDQWSKWICYYDDRKKKKYGSDAINFCVLDDKYKKFCKGGKYTSYNAFFWKWYHDMLHDSVERRELMSCINNAKSQNCKNNEKKNECCGGEKGAFPNATSREKKKGDQWSKWICYYDAASGNCKNNEKKNECCGGEKGAFWYKQKKEKFWEAIKDHFGKQKDIIEGCTGCDAGVTLAAVLKLEFLNEDTEEKS
                                                                                                                                                                                                                                                                                                                   TTKTVRDANLENADQEYKDYKTTQGPSKQGNDYLKDKCDNKKCSCMEGNVLTDVSSKK
PFGI I XHKY SEKCNCLGAKFVPNVPRAPPQPPPPPPAL PAPATTPGVNPCEI I WITLF
SDTNKFKDACTLKYGPKAPTSWKCI FFGNTSLBGARTDSEGSDAKSRHKENDLAPSGS
SDTNKFKDACTLKYGPKAPTSWKCI FFGNTSLBGARTDSEGSDAKSRHKENDLAPSGS
NQGS I CVPPRRKLYVTPLTKWAEETTKGSKSQESGKAEGTSESSGSEASSPGGTSSQ
GEKSPGGLSTPASTSSPSNSRDDDLLKAFVESAAVETFFLWKKYMDKQKELDEKKKQ
GEKSPGGLSTPASTSSPSNSRDDDLLKEFGDI PEEFKROMFYTLGDVBDLLVRGGNT
QRESGCLVGALDGNSGNDDEDKDPGKKLEKGDI PEEFKROMFYTLGDVBDLLVRGGNT
GDSGNTNGSNNNNI V I EASGDKQDEMKKI OKAI DEHI NS LKQAASVPNPQRPGQQQQN
                                  KIEFNEQSETFKHTKHCDPCSSFKIDCRNGKCKSGDTKGKCDGITTIDAKEIAKMISS
TPDVVMRVSDNDTNTFEGDDLKVCEGKGIFKGIRKEEMKCRNECGLDVCGLKKGDNNG
KLDDKQIILIRALIKRWLEYFLEDYNKIKHKISDCINNGEGNICKRDCQNKCNCVGEW
                                                                                                                                                     KKLAQIKVDCKVDSADYKCSGYGEECKIEDISNIGVFADLKCPGCGRECRKYKKWIER
KKIEFGEQKSAYVKQKTKCKEESGGGGNCGTVKTCDTAAQFLERLGPCKNNDNGEG
                                                                                                                                                                                                                                      SSLTRETLMKEHAPSI MEGMI CALTYKENDEKKI VKDNEVYEKFFGTTPGTTSGKYKE
KYEYNTVKLDENSDTEAKDTKATAPSDNTPTFLSHFVLRPPYFRYLEEMGETFCKERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCEVKSGNNYFRATCGDEKNPSLTSKQCRCDKDKAGKPIKGSGNVNIVPTYFDYVPQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GASGDAKNY I DDLKGDLQKAPNI NPKL I GTDDPCKL VEDYYNNHVNGDGKGERY PCTE
LSGKKFQNPPSDTLGGQCTNSKMRSGCEGACAPYRRLHLCHHNLES I ETTSKTASDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Similar to Plasmodium falciparum variant-specific
surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa
fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
I KLKKEEWEKI KKHYLEKNKEGDNDMKSSVRNFLEKFEHR PEFNKA I KPCKGLTQFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLEVCMAAKYEGQSINTHYTKHEHSNKDSPSQLCTVLARSFADIGDIVRGKDLFYGNT
YESARREKLENKLKEVPGKIHGGLSEEAKKKYQDGDGNYYQLREDWWTANRETVWKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="erythrocyte membrane protein 1 (PfEMP1)"
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/db_xref="GI:23498127"
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join(35153. .41725,42757. .44124)
/gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MVRTGGSGGGGVDKDGIDHQSAKHLLDSIGKKVHDQVKNGADGT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="UniProt/TrEMBL:Q8I220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join (35153.
/gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="synonym:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mol_type="genomic DNA"
isolate="3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .347582
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TPIEIEFYLYSDDKQGVITEKLKDFCRGPNNYNDENLQKWKCYNKNGEYNKCEMISWLY
QDPKEYNLMLSVECHISWAKNLLIDTIRWEHQLKNCINTAUTDCTSKCIKNCECYSE
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LDRSNGGTGGIDGCNPKIGNYPSWNCERNESKAENKGACVPPRREKFCVSLLAKEGI
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RAVFKKINDNLKEKEISDYDNDPNYYKLREDMWTANRDQVMRAITCYIPYYVNYFKKT
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complement (join(52002. .53297,54200. /gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKYTKGTIDLLRVINIPKSDVDIPTKLSPNRVIPYTSGKYRGKRVIYLBGDSGTDSGY
TDHYSDITSSSEYEBMDINDIYAPRAPKYKILIEVVLEPSGNNTTASGNNTTASGN
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VPNDYSSGDIPFNTQHNTLYFDKPDEKPFITSIHDRNLYTGEEYNYDMSTNSGNNDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to Plasmodium falciparum variant-specific surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 a/fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (join (52002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMHMM2.0
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/gene="RIF"
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upstream VAR gene PFD0005w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGKONLYSGQNNVYSGIDFTSDNRGLTSGKHDSYSGIDLINDTLSGNQHIDIYDEVLK
RKENELFGTNHVKHTTINRFAKPARDDPLHNQLELFHTWLDRHRNMCEKKNNNKEELLD
KLKEEWENETHSGNTHPSDSNKTLNTDVSIQIDMDNPKPINQFTNMDINVDTPTMDNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="erythrocyte membrane protein 1 (PfEMP1)"
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/db_xref="GI:23498129"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                  CCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAGGGA 1043
                                                                             TTTTTTTTTTTTTAATTTGAAATATATTTATTTTATTTTCTACATATAAAAAAATA
                                                                                                    TTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAA
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EKTDICKLKNFNDKIDLNQYTTFKVFLEYWLQDFIEGYYILKKRKIIEQCKENGGETC
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Pred. No. 0.00048;
0; Mismatches 341;
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Best Local (
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                          TTTNAAAAATAATTTTATANTTATNNAANANAAATTTAAAANTNAANANAAAATTTTA
                                                  TGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCT 1018
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Matches 275; Query Match Best Local :

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813 TANAAATTTTTINAAAAACTAATTNTAANNATANTNAATTTTTNTAAAAAAANNNAAAAA
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapo of breast cancer
Patent: WO 0151628-A 7675 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ422641
Sequence 7675 from Pate:
CQ422641
CQ422641.1 GI:41374870
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                        TTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGA 898
NNANATTAAAAAATTTATTTTTTTTANTTCTATAAAATTAAAANAANAANAATAAAATAAT
                                                                                   CTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAA
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 0.00065;
0; Mismatches 367
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PZA01377 CML247 Zea mays
tagged site.
BV119878
BV119878.1 GT:45589251
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Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
ABI protocol - using with ampliTaq DNA polymerase FS
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA amplification
RedTag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
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1 (bases 1 to 241)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR amplification of genomic DNA
Template: 50 ng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bgaut@uci.edu
Primer A: TTCTACGTCCAAATGCATCAAAGA
Primer B: AGGAAACCAAGCCTTATGAGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
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(949) 824-2181
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                                                                 /clone_lib="Zea mays CML247"
/dev_stage="seedling"
/note="Organ: leaf; genomic
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                     mol_type="genomic DNA"
cultivar="CML247"
                                                                                                                                                                                                                                                                                              organism="Zea mays"
                                                                                                                                                                                  db_xref="taxon:4577"
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                                           ACTGTTAATTTÄGTTCCAATATCCATCACCAAGGATGGATATCCTAACCGCATATCTTGT
                                                                  ATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTAT 978
                                                                                         ATTTTCCCTTGGGAAAATAGAAATCCCAAGGGAAAATGGAGTTCCCAAACTAACCCTAAT 76
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Search completed: September 16, 2005, 03:01:11 Job time : 4684.65 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result		Query				
NO.	Score		Length	BB	Ħ	Description
1	1394	100.0	1394	2	AAX07408	Aax07408 Zea mays
ผ	1394	100.0	1394	v	AAH76332	2
u	1389.2	99.7	1394	N	AAX07409	Zea mays
4	1389.2	99.7	1394	v	AAH76333	
ហ	238.8	17.1	255	ហ	AAH76340	Z. mays
6	146	10.5	158	ហ	AAH76334	
c 7	70.2	5.0	683	4	AAL15210	Aal15210 Human bre
ი 8	70.2	ი	960	片	ACN85231	Acn85231 Breast ca
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c 11	66.4	4.8	6027	N	AAX58751	Aax58751 Maize du
c 12	66.4	4.8	6027	æ	ABX09935	Abx09935 DNA encod
	66.4	4.8	6027	12	ADK12106	Adk12106 cDNA enco
14	66.2	4.7	439	œ	ABX35844	Abx35844 Bovine ES
	65.6	4.7	346	4	AAI87279	Aai87279 Human pol
c 16	65.6	4.7	8056	œ	ABZ10246	Abz10246 Haematopo
c 17	64.6	4.6	9859	13	ADS89714	Ads89714 Oligonuc
c 18	64.4	4.6	9859	13	ADS89440	Ads89440 Oligonuc
c 19	64	4.6	8056	8	ABZ10100	Abz10100 Haematopo
20	63.8	4.6	431	œ	ABX44556	Abx44556 Bovine ES

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
58.6	58.6	58.8	59	59	59.2	59.2	59.4	59.4	60.2	60.2	60.4	60.4	60.6	60.6	61.4	62.4	63	63.4	63.4	63.4	63.4	63.4	63.6	63.6
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	5	5	5	5	5	5	5	4.6	4.6
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ACN56029	ADL43653	ABX39417	ABL32871	ACN56273	ABL70528	ABK31213	AAS46506	ADL43834	ABN80326	AAS46636	ADL38222	ADI73089	ABL33097	ACN56344	ABL32909	ABL92322	ABL34113	ABN80285	ABK28424	ABL34085	AAS46779	AAS45494	AAI61372	AAI61371
Acn56029 Cotton an	Adl43653 Human ova	Abx39417 Bovine ES	Abl32871 Human imm	Acn56273 Cotton an	Abl70528 Chemicall	Abk31213 Signal tr	Aas46506 Tumour su	Adl43834 Human ova	Abn80326 Human che	Aas46636 Tumour su	Adl38222 Human ova	Adi73089 Human ova	Abl33097 Human imm	Acn56344 Cotton an	Abl32909 Human imm	Ab192322 Chemicall		Abn80285 Human che	Abk28424 DNA trans	Ab134085 Human imm	Aas46779 Tumour su	Aas45494 Chemicall	Aai61372 Soybean 2	Aai61371 Soybean 2

ALIGNMENTS

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RESULT 1
AAX07408
Ms45; male; tissue-preferred; plant tissue; differentiated;
                                                                                                                                                                                                                                                                            AAX07408 standard; DNA; 1394 BP.
                                                                                                   WPI; 1999-105628/09.
                                                                                                                 Albertsen MC,
                                                                                                                                                         19-JUN-1998;
                                                                                                                                                                       30-DEC-1998.
                                                                                                                                                                                     WO9859061-A1
                                                                                                                                                                                                  Zea mays.
                                                                                                                                                                                                                                    Zea mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                  08-JUN-1999
                                                                                                                                                                                                                                                               AAX07408;
                                                                                                                                           23-JUN-1997;
                                                                                                                              (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                           97US-00880499.
                                                                                                                Fox TW,
                                                                                                                                                         98WO-US012895.
                                                                                                                 Garnaat CW,
                                                                                                                                                                                                               regulatory region; plant cells; maize; hybrid seed; fertility; ss.
                                                                                                                 Huffman GA,
                                                                                                                 Kendall
                                                                                                                 TL;
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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue-preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants

New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.

Claim 2; Page 22-23; 39pp; English.

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94; Conservative
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              GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
                                                   TGCCAGACTAGCCCTAGAATGTTTTTCCCAATAAATTACAATCACTGTGTATAATTTAGTTTG
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                                   TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG
                                                                                    TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT
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AAH76332 standard; DNA; 1394 ΒP

AAH76332;

29-OCT-2001 (first entry)

Z. mays M845 male tissue-preferred regulatory region encoding

regulatory region; transcription;

male

fertility;

Ms45; male tissue; hybrid seed; ds.

WO200160997-A2

23-AUG-2001

13-FEB-2001; 2001WO-US004527

2000US-00504487.

15-FEB-2000;

(PION-) PIONEER HI-BRED TNI

Albertsen М О Fox ŢW, Garnaat č, Huffman ຸດ

Kendall

2001-514772/56.

A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant. comprising nucleotide the MS45 gene useful f for

Claim 4; Page 46; 50pp; English.

RESULT 2
AAH76332
ID AAH7
XX AAH7
XX AAH7
XX AAH7
XX Ms45
XX Ms65
XX Ms66
XX Cla
XX The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The the of.

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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably

Claim

3; Page 23-24; 39pp; English.

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Similarity 99.8%;
91; Conservative
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                               ATGACTATAAAGTCATTTTTATATAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC
                                                                                                                                           ATTGTTTTTATAAATTTTCTTCTTTCTTTCTTACAATAGAGTGATTTTTCTTCCGATTTTATAAA
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Pred. No. 5.6e-290;
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                                                                                                                               A male tissue-preferred regulatory region comprising nucleotide essential for initiating transcription of the MS45 gene useful f mediating fertility in a male plant.

 mays Ms45

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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a

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                                                        CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA
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TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGAGT
                   TTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT
                                                                                                                                                                                          ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA
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99.8%;
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Pred. No. 5.6e-290;
0; Mismatches 3;
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription

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                               A male tissue-preferred a essential for initiating mediating fertility in a
                                                                                                                                                                         M845;
                                                                                                                            23-AUG-2001
                                                                                                                                                                  hybrid seed;

 mays Ms45

                                                                                                                                                                                                    29-OCT-2001
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                                                                                                                                                                         male tissue; regulatory region; transcription; male fertility;
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                                                                                                                                                                   promoter;
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                                                                       , W.I
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                               regulatory region g transcription of a male plant.
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                                                                       Huffman
                                      comprising nucleotide the MS45 gene useful f
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                                                                       Kendall
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Best Local S
Matches 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the MS45 gene. A method of mediating male fertility in a plant is a provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. I present sequence represents a Z. mays Ms45 promoter fragment
                  The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is
                                                                                                                                                                                    essential
                                                                                                                                                                                                       A male
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mes 243; Conserv
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                                                                                                                                                        tissue-preferred regulatory region ial for initiating transcription of ing fertility in a male plant.
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  gene. A method
that involves i
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                                                                                                                50pp;
                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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Pred. No. 7.5
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    an expression
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                                                                                                                                                                                comprising nucleotide sequences the MS45 gene useful for
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
                                                                                         The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting discussing engineers for the total discussing markers for the polynucleotides and encoded polypeptides are potential markers for the polynucleotides.
detecting, diagnosing, monitoring, characterising treating and obtentially preventing breast cancer. The polymucleotides and opolypeptides are also useful for isolating compounds with cytoactivity
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Pred. No. 7.1e-22;
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Best Local Sim
Matches 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM
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                                                                                                                     GTTGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATT
                                                                                                                                                      NNANATTAAAAAATTTATTTTTTTANTTCTATAAATTAAAANAANANNAATAAAATAAT
                                                                                                                                                                                                                                             ANATGACTATANAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAA
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                                                          TGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCT
                                                                                        TTTNAAAAATÄATTTTATANTTATNNAANANAAATTTAAAANTNAANANAAAATTTTA
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39.2%;
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0; Mismatches
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2.6e-05;
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The present invention describes an isolated polynucleotide comprising a CC first, second, third, fourth or fifth nucleotide sequence, or their CC complement encoding a polypeptide either having flowering locus T gene CC (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also CC described: (1) a vector comprising the polynucleotide; (3) transforming a cell by transforming a cell with the polynucleotide; (3) transforming a cell by CC transforming a cell with the polynucleotide; (4) a cell comprising the CC recombinant DNA construct; (5) producing a plant comprising the transformed plant cell; (6) a plant comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (8) an CC isolated polynucleotide comprising a first nucleotide sequence is comprising a first nucleotide, where the Cfirst nucleotide sequence is comprised by another polynucleotide, where the other polynucleotide includes the second, third, fourth, fifth or CC sixth nucleotide sequence; (9) an isolated polypeptide having FT or Ap3 construct on the polynucleotide sequence; (9) an isolated polypeptide having FT or Ap3 construct on the polynucleotide comprising isolating the polypeptide from a CC encoded by the polynucleotide above; and (10) isolating a polypeptide containing a recombinant DNA construct comprising the polypucleotide polynucleotide sequence; (9) an isolated polynucleotide save useful containing a recombinant DNA construct comprising the polypucleotide containing a recombinant DNA construct comprising the polynucleotide comprising isolating the polynucleotide operably linked to a regulatory sequence. The polynucleotides are useful contained to the rate of cell division to enhance contribe sequence from the present sequence and tissue culture morphology and the rate of cell division to enhance contained to the present sequence represents an FT homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3) homologs, useful for floral development, e.g. engineering plant flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danilevskaya O, Hermon P, Brı
Rafalski JA, Sakai H, Cahoon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; SEQ ID NO 63; 109pp; English.
                                            sequence from the present invention.
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oon E, Cahoon R,
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Query Match

Score 69.8;

DB 13;

Length 13400

2695 G; 3795 T; 0 U; 0 Other

Sequence 13400 BP; 3962 A; 2948 C;

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The present sequence represents the P-Ztap promoter of maize. It is used CC in the method of the invention. The specification describes a method for the production of male sterile plants. The method comprises selective expression of DNA encoding a protein that causes tolerance to glyphosate CC and application of glyphosate. The method uses two DNA molecules, each CC operably linked to a separate promoter, whereby the first promoter CC functions in plant cells to produce a protein that causes tolerance to glyphosate, and the second promoter functions in plant cells to cause the production of a second RNA sequence in a male reproductive tissue. Expression of the DNA promotes tolerance to glyphosate in those tissues in which it is expressed. Expression of the second DNA molecule causes the production of an RNA sequence which can inhibit the glyphosate collerance generated by expression of the first DNA molecule. By using a CC promoter for the second DNA molecule which restricts the production of the antisense RNA to only a subset of the tissues which express the first DNA molecule, only the subset of tissues which the second DNA molecule is expressed will be susceptible to glyphosate toxicity. In this way, a specific cell type or combination of cell types, depending upon the promoters utilized, can be selectively ablated by application of cell undesirable crop outcrossing, and for lengthening flower life. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1A-B; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTAGCCCTAAA 2013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCTTTTAAGGGCTAGTTTGGGAACCACATTT-TTCCAAGGGATTTCAATTTTCGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     655.
                                                                                                            /note= "functional fragment of cDNA specifically claimed in Claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                               2425.
                                                                                                                                                                                                                                                                                                                                                                             /note= "functional
in Claim 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                  n Claim 17"
                                                                                                                                                                                                                       note= "functional
                                                                                                                                                                                                                                                                   1438. .2424
                                                                                                                                                                                                                                                                                                               /*tag= e
/note= "functional
                                                                                                                                                                                                                                                                                                                                                      1369. .1944
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n Claim 14"
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/note= "functional
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/note= "functional fragment of cDNA specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSII; DU1; dull1 gene; maize; transgenic plant;
                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
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                                                                                                                                                                                                                                                                                        Claim 15"
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74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                  fragment
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                                                                                                                                                                                                                                                                                                                                                                                                    of cDNA specifically claimed
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                                                                                                                                                                                                                                                                                                            cDNA specifically claimed
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RESULT 12
ABX09935/c
ID ABX099
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for a 186 kDa protein extremely similar to potato tuber starch synthase SSIII. Its expression pattern indicates that Dul codes for SSII of maize endosperm. The Dul product contains unique sequence features in its N-terminus that may mediate direct interactions with other starch biosynthetic enzymes. Mutations within the maize SSII gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthase(s), starch branching enzyme(s) and possibly starch debranching enzyme(s). The isolated cDNA can be used to provide an enzyme with which to regulate the production of starch, and with which to regulate the production of starch, and with which to produce altered or novel forms of starch, e.g. in transgenic plants. Expression of Dul in bacteria and yeasts also modifies glycogen production. Claimed expression vectors comprise the cDNA or fragments of it that code for functional portions of DUI
                                                                                                                                                        LINKR; glucosyl transferase domain; GLYTR; C-terminal granule bound starch synthase; GBSS; morphology; retro
                                                                                                                                                                         Starch; starch synthase; glucan association domain; GLASS; linker LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the nucleotide sequence of the maize gene dull1 (du1). To illustrate the role of the du1 locus in starch biosynthesis, a transposor tagging strategy was used to isolate the gene and describe its polypeptide product. The invention reports tagging of the du1 locus with Mu transposon, cloning and characterisation of a portion of the gene, and isolation a near full-length cDNA (the present sequence). The amino acid sequence (see AAY06199) deduced from this cDNA indicates that Du1 codes
                                                                                                                                                                                                                                DNA encoding maize Starch synthase III (Dul).
                                                                                                                                                                                                                                                                      17-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6027 BP; 1800 A; 1177 C; 1441 G; 1609 T; 0 U; 0 Other;
                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                        ABX09935;
                                                                                                                                                                                                                                                                                                                                            ABX09935 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding starch synthase enzyme of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-327406/27.
                                                                                                                                       waterbinding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACGGGCTAGTTTGGGAACCCCCATTT-TTCCAAGGGATTTCCATTTTTCCAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 104-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                           DNA; 6027
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77.5%;
                                                                                                                                        potential;
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                                                                                                                                                                                                                                                                                                                                              ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66.4; DB 2
Pred. No. 0.00028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                          retrogradation;
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29-MAR-2002; 2002WO-US009574.

10-OCT-2002

WO200279410-A2

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RESULT 13
ADK12106 standard; cDNA; 6027 BP
XX
AC ADK12106;
XX
DT 03-JUN-2004 (first entry)
XX
DE cDNA encoding maize starch synth
XX
Maize; dull 1; DU1; starch synth
XX
Maize; dull 1; DU1; starch synth
XX
Maipha-1,4-glycosyltransferase c;
XX
alpha-1,4-glycosyltransferase c;
XX
plant; gene; ss.
XX
CS Zea mays.
XX
XX
Sea mays.
XX
XX
FM (CDS 120.5148
FT CDS 120.5148
FT CDS 120.5148
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PN US2004049810-A1.
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1-MAR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                   Maize; dull 1; DU1; starch synthase; alpha-1,4-glycosyltransferase cataly
                                                                                                                                                                                                                                                                                         cDNA encoding maize starch synthase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6027 BP; 1800 A; 1177 C; 1441 G; 1609 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding fusion protein consisting of 4 different functional domains selected from glucan association domain, linker domain, glucosyl transferase domain, and C-terminal end, useful for producing modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5606 TCTACGGGCTAGTTTGGGAACCCCATTT-TTCCAAGGGATTTCCATTTTTCCAAGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 225-227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                    Location/Qualifiers
                                                                                     /product= "DU1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.8%;
77.5%;
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                                                                                                                                                                                                                                   catalytic activity; starch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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RESULT 14
ABX35844
ID ABX35
XX ABX35
AC ABX35
XX 20-FE
XX BOVIN
XX BOVIN
XX BOVIN
XX Gene
OS BOS T
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XX 11-Ja
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Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of a maize gene, dull 1 (DUI), and the polypeptide it encodes. The DUI polypeptide has starch synthase activity, and comprises an N-terminal arm region, a C-terminal catalytic region, and a region of about 900 amino acids terminating with the catalytic region. The C-terminal catalytic region has a catalytic domain comprising alpha-1,4-glycosyltransferase catalytic activity. The dul polynucleotide sequence is useful in producing starch e.g. from a transgenic plant or transfected cell. The present sequence encodes maize
                        (BYAT/)
(MATH/)
(TAON/)
                                                                                                                                                                                                                                                                                                                                                                                                               gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                       24-SEP-2001; 2001US-00960352
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                                                                                                                                                                                                                                                                                                                                                                 Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine EST
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                                                                                                                            12-JAN-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                             26-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-238526/22
P-PSDB; ADK12117.
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  (WARR/)
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(JAME/) JAMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                        MATHIALAGAN TAO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production.
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  WARREN W C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTACGGGCTAGTTTGGGAACCCCATTT-TTCCAAGGGATTTCCATTTTTCCAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with lactation/muscle/fat deposition #1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                            99US-0115707P.
2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 439
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77.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66.4; DB 12;
Pred. No. 0.00028;
0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             identification;
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RESULT 15
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Best Local Simi
Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and control of the the mRNA molecule; and comprising: (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition
                   06-NOV-2001
                                                                                          AAI87279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 439 BP; 45 A; 51 C; 56 G; 286 T; 0 U; 1 Other;
                                                       AAI87279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-110599/10
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                                                                                                                                                                                                                                                                                                                                                           746 AGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                           242
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATTTTTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTATATACATTTTTCTTCT
                                                                                          standard;
                                                                                                                                                                                     TTCTTTA 428
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                   (first entry)
                                                                                          CDNA; 346 BP
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54.3%;
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Pred. No. 0.
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Best Local Sim:
Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                   production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/ninhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 346 BP; 188 A; 22 C; 16 G; 120 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haemator tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 7339; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                 989
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94
                        CTTACAATAGAGTGATTTTCTTCCGATTTTAT 717
                                                                    GACTTATATATATATATAAATTTTTTTTTTTTAGAAAATAATTTACATTTAAACAATAAAAA
                                                                                                                                                                                                                                    GAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAAAT 565
                                                                                                                                                                                                                                                                      AGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAATGTTTAAA 505
                                                                                                                                                                   TATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGACG
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                                                                                                                                                                                                                                                                                                                                         Conservative
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52.6%;
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Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                         Mismatches
 63
                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 346;
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Search completed: September 15, Job time: 679.892 secs

2005, 21:33:03

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                1394
1389.2
66.4
66.4
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99.7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1202784 segs, 818138359 residues
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1394
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10817.505 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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4.2 2523

4.1 19124

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               US-08-968-542C-1

US-09-554-467A-1

US-09-513-294A-5397

US-09-313-294A-5397

US-09-313-294A-5397

US-08-880-499-2

US-08-880-499-2

US-09-806-708B-23

US-09-806-708B-23

US-09-640-173-53

US-09-640-173-53

US-09-713-550-53

US-09-913-550-53

US-09-913-550-53

US-09-9149-116-15129

US-09-913-916-15129

US-09-9149-016-15348

US-09-949-016-15348

US-09-949-016-15350

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US-08-880-499-2
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Sequence 1, Appli
Sequence 2, Appli
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Sequence 1, Appli
Sequence 13, Appli
Sequence 1357, Ap
Sequence 1357, Ap
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Sequence 53, Appl
Sequence 15129, A
Sequence 1, Appli
Sequence 15318, A
Sequence 15318, A
Sequence 15318, A
Sequence 1530, A
Sequence 1530, A
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US-08-880-499-1
               Matches 1394;
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Best Local Similarity
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47.8	49.2	49.2	49.6	49.8	49.8	49.8	50	50.2	50.2	50.4	50.6	50.6	50.6	51	51.4	51.4	51.6
3.4 601	3.5 126176	3.5 126176	3.6 640681	3.6 266293	3.6 231129	3.6 2435	3.6 1392	3.6 317366	3.6 832	3.6 731		3.6 16573	3.6 1039	3.7 601	3.7 129415	3.7 50383	3.7 134987
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US-09-949-016-25787	US-09-949-016-16138	US-09-949-016-16137	US-09-790-988-1	US-09-949-016-11934	US-09-949-016-16110	US-09-306-593-1	US-09-257-584-1	US-09-949-016-16001	US-09-621-976-2813	US-08-451-405A-2	US-09-949-016-14164	US-09-949-016-14876	US-09-902-540-1280	US-09-949-016-156535	US-09-949-016-16997	US-09-949-016-17600	US-09-949-016-15509
Sequence 25787, A	Sequence 16138, A	Sequence 16137, A	Sequence 1, Appli	Sequence 11934, A	Sequence 16110, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 16001, A	Sequence 2813, Ap	Sequence 2, Appli	Sequence 14164, A	Sequence 14876, A	Sequence 1280, Ap	Sequence 156535,	Sequence 16997, A	Sequence 17600, A	Sequence 15509, A

ALIGNMENTS

; Sequence 1, Application US/08880499 Patent No. 6037523 ; GENERAL INFORMATION: APPLICANT: Albertson, Marc C. APPLICANT: Fox, Tim W. APPLICANT: Carl, Garnaat W. APPLICANT: Huffman, Gary A. APPLICANT: Kendall, Timmy L. TTITLE OF INVENTION: MAIE TISSIE-DE ; MOLECULE TYPE: US-08-880-499-1 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800 TELEPAX: (515) 248-4844 INFORMATION FOR SEQ ID NO: 1: ZIP: 50131 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 1394 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear APPLICATION NUMBER: US/08/680,499 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 0578 CORRESPONDENCE ADDRESS: ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AND METHOD OF USING SAME STREET: Darwin Bu: STREET: Box 1000 CITY: Johnston STATE: Iowa COUNTRY: USA TO E0121 NUMBER OF SEQUENCES: DNA (genomic) #1.30

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100.0%; Score 1394; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches

Mismatches

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                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499

FILING DATE: CONCURRENTLY HEREWITH

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Sweeney, Patricia A.

REGISTRATION NUMBER: 0578

TELECOMMUNICATION INFORMATION:

TELEPAX: (515) 248-4800

TELEPAX: (515) 248-4844

INFORMATION FOR SEO ID NO: 2:
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Patent No. 6037523
GENERAL INFORMATION:
Query Match 99. Best Local Similarity 99. Matches 1391; Conservative
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APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
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                                                               TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG
                                                                                                TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT
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       TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAGAAATCAGTTTTAAGTCATTGTCCC
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TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC
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DESCRIPTION: CONA to mRNA HYPOTHETICAL: no ANTI-SENSE: no ORIGINAL SOURCE: ORGANISM: maize TISSUE TYPE: endosperm	LENGTH: 6027 bp TYPE: nucleic acid STRANDEDNESS: double-stranded TOPOLOGY: linear MOLECULE TYPE:	TELECOMMUNICATION INFORMATION: TELEPHONE: (713) 777-2321 TELEPAX: (713) 777-6908 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:	ITTORNEY/AGENT INFORMATION: NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423 REFERENCE/DOCKET NUMBER: D6036	H	intosh ord 6.0.1 : S/08/968,	ER READABLE FOR UM TYPE: 3.5 f UTER: Apple Ma	CITY: Houston STATE: TX COUNTRY: USA ZIP: 77071	CORRESPONDENCE ADDRESS: ADDRESSEE: McGregor & Adler, LLP STREET: 8011 Candle Lane	APPLICANT: Myers, et al. TITLE OF INVENTION: dull1 Codes For A No. 5981728el Starch TITLE OF INVENTION: Synthase NUMBER OF SEQUENCES: 35	RESULT 3 US-08-968-542C-1/C ; Sequence 1, Application US/08968542C ; Patent No. 5981728 ; GENERAL INFORMATION:	1381 CGTCCACCATG 1394 1381 CGTCCACCATG 1394	1321 AAAGATCACAACAGCTAGCGTTCTCCCGCTAGCTTCCCTCTCCCTCTGCCGATCTTTT 1380	CCATCTTACTCATGCAACTTCCATGCAAACACACGCACATATGTTTCCTGAACCAATCCATT 132	1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260 	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200	1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140

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RESULT 5
US-08-410-784A-3/c
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FILE REFERENCE: D6036PCT
CURRENT APPLICATION NUMBER: US/09/554,467A
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/US98/24225
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 08/062,102
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-554-467A-1/c
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                                        PALEENT NO. 5914-1.

PALEENT NO. 5914-1.

GENERAL INFORMATION:

APPLICANT: MYERS, ALAN M.

APPLICANT: JAMES, MARTHA G.

APPLICANT: JAMES, MARTHA G.

TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING TITLE OF INVENTION: SUGARY 1

TITLE OF INVENTION: SUGARY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 93; Conserv
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LENGTH: 6027
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                              Sequence 3, Application US/08410784A Patent No. 5912413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application Patent No. 6639125 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Myers, Alan M.
APPLICANT: James, Martha G.
APPLICANT: James, Martha G.
TITLE OF INVENTION: dull1 Coding for a No. 6639125el Starch Synthase and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: cDNA sequence corresponding OTHER INFORMATION: starch synthase enzyme DU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: maize
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STREET:
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LIBRARY: (gtll
CLONE: pmgf10; pmg6Aa; pmgt6-2M
                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                             5606
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                                                                                                                                                                                                                                                                                                                                                      852 TTAGTTTATTTTCTCTTTTATAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
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                  3: Weingarten, Schurgin, Gagnebin and Hayes LLP
Ten Post Office Square
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77.5%;
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Pred. No. 2.2e-06;
0; Mismatches 26;
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Pred. No. 2.2e-06;
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US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
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Best Local Similarity
Matches 105; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 2523 base pairs
                                                                                                                                                             APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H
APPLICANT: Peterson, David
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
MEDIUM TYPE: TBM Compat
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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NAME: Heine, Ph.D., Holliday C
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 15U-0C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
NUMBER OF SEQUENCES: 4
                                                                                                                     APPLICANT: Peterson, David S. APPLICANT: Su, Xin-zhaun FLARPLICANT: Wellems, Thomas E. TITLE OF INVENTION: BINDING DUTITLE OF INVENTION: AND PLASM
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    774 AAAAATCITTCTGATTITTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTT 833
                                                                                                                                                                                                                                                                                                                                                                                                     ATAGAGTTTACAAACTAGTCTTAAAAT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGAGTTGCCAGACTAGCCCTAGAAT 920
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                                                   E: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
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                                                                                                                           BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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Pred. No. 0.00013;
0; Mismatches 39;
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; TOPOLOGY: lin
; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-487-826B-13
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                                             GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN |
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 5397
LENGTH: 279
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.1%;
Best Local Similarity 50.2%;
Matches 141; Conservative
                                                                                                                                                                                                                                                             Sequence 5397, Application US/09313294A Patent No. 6476212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 1
                              ORGANISM: Zea maye
NAME/KEY: misc_feature
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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HER: NI
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Pred. No. 0.00073;
0; Mismatches 140;
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SEQ ID NO 1357
LENGTH: 612
                                                                                                                                                                                                                                                                                                                                         Matches 127;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
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NAME/KEY: unsure
LOCATION: (1)..(612)
OTHER INFORMATION: unsure at all n locations
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LOCATION: 10, 12, 185-186, 204, 253, 27,
OTHER INFORMATION: a, t, c, g, or other
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                                 866 CTTTATA 872
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                                                                                                                                                                                                                                                                                                       626 TTCAGATTTTTCTTTTTCATTCTTATTTTTGTTATTGTTTTTTATATACATTTTCTTCT 685
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Similarity 69.0%;
TATTTTA 314
                                                                   ATTTTTTTTTTTTTTTTTTTTTTTTATTTTTT
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Pred. No. 0.00043;
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Pred. No. 0.00029;
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RESULT 10
US-08-880-499-2/c
; Sequence 2, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
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Patent No. 6037523
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: Bingle
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REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Albertson, I
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garna
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NAME: Sweeney, Patricia
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
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Pred. No. 0.0006;
0; Mismatches 84;
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; MOLECULE TYPE: DNA (genomic)
US-08-880-499-2
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US-09-806-708B-23
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Sequence 23, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
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Best Local Similarity 55.8%;
Matches 106; Conservative
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TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, 'CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITY
CLASSIFICATION: 800
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
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NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,73
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 50131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830
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Huffman, Gary A.
Kendall, Timmy L.
Kendall, Kenda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fox, Tim W. Carl, Garna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albertson, Marc C.
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Pred. No. 0.0006;
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; LOCATION: (1)...(1055)

; OTHER INFORMATION: consensus sequence of A.t.

US-09-806-708B-23
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 23
LENGTH: 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.0%; Score 55.4; DB 4; Best Local Similarity 22.5%; Pred. No. 0.0006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 182; Conservative 181; Mismatches 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence FEATURE:
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                                    AAATCAGTTTTAAGTCATTGTCCCTGAG 1084
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                                                                                                            AYARAAAYTTRTANNGACTTTTTTNNTTGGMRTNTAAARGWANNNNNNNNNNNNNNNNNGACWA 756
                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTAAGAGCTAGTTTGGCAACCCTG
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KNNTTMCWTCKAWMKAWATGAATTTNAG
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                                                                        WRTTTATANCGTNNNNNNNNNNAYATTTNTATTTTWWRTRKANNNNNNNAAAYYGAAAW
                                                                                                                                                                                        ACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAAT
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844
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RESULT 13
US-09-640-173-53
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US-09-004-056-1/c
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APPLICANT: Calgene LLC
TITLE OF INVENTION: Plant Expansin Promoter Sequences
FILE REFERENCE: 125
CURRENT APPLICATION NUMBER: US/09/004,056A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 60034914
EARLIER APPLICATION NUMBER: 60034914
EARLIER FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
                                                                                                                        Sequence 53, Application US/09640173
Patent No. 6613515
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 2614
TYPE: DNA
ORGANISM: GOBBYPium
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Best Local Similarity
Matches 155; Conserv
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TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: promoter
LOCATION: (947)
OTHER INFORMATION: unknown
FEATURE:
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NAME/KEY: promoter
LOCATION: (930)
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milarity 54.2%;
Conservative
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Pred. No. 0.00095;
0; Mismatches 128;
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SOFTWARE: SEQ ID NO 53

FastSEQ for Windows Version 3.0

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OV.
FILE REFERENCE: 210121.484C4
CURRENT APPLICATION NUMBER: US/09/713,550
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 205
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
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                                                                                 S
                                                                                                                                                                  ; ORGANISM: Homo sapien
; FEATURE;
; NAME/KEY: misc feature
; LOCATION: (1):..(396)
; OTHER INFORMATION: n = A,T,C
US-09-713-550-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-713-550-53
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n = A,T,C
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                 ATAGAGTGATTTTCCTTCCGATTTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCA
                                                                        TTTTTCTTTTTCATTCTTGTTATTTTGTTATTTTTTTATATACATTTTCTTCTCTTACA
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AATTCANAAAAAGAANAAGAAAANATAANANNNANCNNANNNNNNNNATNNTNCTTNATA 310
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ilarity 43.8%;
Conservative
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Pred. No. 0.00052;
0; Mismatches 178;
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CA
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
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Matches 139
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NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C
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NTNNTTNNNNNANNGGG 327
                                                                                                                       CGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTGGCAA 811
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Pred. No. 0.00052;
0; Mismatches 178
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Search completed: September 15, 2005, 08:24:54 Job time : 214.859 secs This Page Blank (uspto)

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Database
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                    Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

22: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

25: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

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10230.248 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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74	78.8	80.8	146	238.8	1389.2	1394	Score
5.3	5.7	5.8	10.5	17.1	99.7	100.0	Query Match Length DB ID
320	1663	1261	158	255	1394	1394	Length
18	20	20	20	20	20	20	80
US-10-425-114-23340	US-10-739-930-1857	US-10-425-115-134230	US-10-713-381-3	US-10-713-381-9	US-10-713-381-2	US-10-713-381-1	ength DB ID
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US-10-425-115-21012	- 1	-10-425-11	3-126-	-10-425-115-	-10-425-114-	-425-114-	-10-425-115-177	-10-425-114-207	60-352-10	-10-425-	-10-109-048	-10-634-262	-10-425-	-10-425-114	-10-425-115	-10-425-114	-10-425-115	-10-425-114-	-10-425-115-	-10-425-115-	-10-425-114-	-10-425-115-4716	-10-425-	-10-425-115-	-10-343-477A-6	-10-198-846-	-10-425-	-10-425-114-	US-10-425-115-52216	-10-425-114-	-10-425-115-	4	-10-425-115-	US-10-425-115-83293	-10-425-114-324	US-10-425-115-141826	979T-#TT-C7#-UT-
Sequence 21012, A	equence 30824,	equence 15082	e 386,	ce 162957,	ce 830,	ce 777,	e 1779	ce 2073		equence 4158	equence 1145, A	equence 1, Appl	e 20264	equence 16607,	equence 14930	e 30881	equence	equence 17816,	equence	equence 75310,	equence 24656,	equence 47165,	equence 4041,	e 87756,	equence	e 6381, A	52219,	31061,	equence	equence	equence 14285	e 17816,	equence 5147	e 83293,	equence 324	equence 1418	education to so

ALIGNMENTS

RESULT 1 US-10-713-381-1

Sequence 1, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:

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; TYPE: DNA; Cea mays; ORGANISM: Zea mays
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Query Match 100.0%; Score 1394; DB 20; Best Local Similarity 100.0%; Pred. No. 1.1e-294; Matches 1394; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR PILING DATE: 1997-06-23
NUMBER OF SEC IN NO. 24-24
NUMBER OF SEC IN NUMBER SEC IN NUMBER OF SEC IN
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARMAT, CARY
APPLICANT: GARMAT, CARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
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Sequence 3, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION SUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
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US-10-713-381-9
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Best Local Similarity 97.2%;
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: USING SAME
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US-10-425-115-134230
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; ORGANISM: Zea mays
US-10-713-381-3
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Sequence 1857, Application US/10739930
Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: KOVALIC, DAVIG K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53377)B
FULE REFERENCE: 38-21 (53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: LA ROSA, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 134230

LENGTH: 1261

TYPE: DNA
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Best Local Similarity 99.4%;
Matches 157; Conservative
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78.2%;
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Pred. No. 5.3e-22;
0; Mismatches 0;
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Pred. No. 2.7e-07;
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RESULT 8
US-10-425-114-16264
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US-10-739-930-1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 23340
LENGTH: 320
Sequence 16264, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Matches
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity
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Publication No. US20040034888A1
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SEQ ID NO 1857
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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Local Similarity 97.6%;
nes 80; Conservative
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                                                                                                                                         182 GCCCTTAATT 191
                                                                                                                                                                                                                                                                                             62 TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA 121
                                                                                                                                                                                                                                                                                                                                                                         95;
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Pred. No. 8.3e-07
0; Mismatches
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APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David APPLICANT: Screen, Steven

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Sequence 141826, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Ross, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 141826

LENGTH: 1326
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US-10-425-115-141826
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US-10-425-114-16264
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16264
LENGTH: 624
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Best Local S
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ORGANISM: Zea maye
                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                   1150 ATTT-TTCCACTGGATTTTCATTTTCCTAAGGAAAATTÄGTTCATTTTCCCTTGÄGÄAAA
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TAGGAATCCCTTAGAAAAAAATAGTTTCCAAACTAGCCCTAAAAT 1253
                                                                                                                              GTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTTATAAAA
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                                      TAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAAT 920
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Pred. No. 5.8e-06;
0; Mismatches 35
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Pred. No. 1.4e-05;
0; Mismatches 50;
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; OTHER INFORMATION: Clone ID: MRT4577_175978C.1
US-10-425-115-83293
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 83293
LENGTH: 2729
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 83293, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
Best Local Similarity 60.7%;
Matches 136; Conservative
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SEQ ID NO 32493
LENGTH: 2445
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
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CURRENT FILING DATE: 2003-04-28
                                                                                                                                                           FEATURE:
NAME/KEY: unsure
LOCATION: (1).. (2729)
OTHER INFORMATION: unsure at all n locations
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ORGANISM: Zea mays
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les 106; Conserv
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ilarity 73.6%;
Conservative
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                                   Score 72.8; DB 20;
Pred. No. 2.2e-05;
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Pred. No. 2.1e-05;
0; Mismatches 37
              Mismatches
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                                                      Length 2729;
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RESULT 13
US-10-425-114-17816/c
Sequence 17816, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
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Best Local S
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 51470
LENGTH: 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 102;
  APPLICANT:
APPLICANT:
TITLE OF IN
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LOCATION: (1)..(1203)
OTHER INFORMATION: unsure at all n locations
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ORGANISM: Zea mays
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  OF INVENTION: Nucleic Acid
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76.1%;
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Pred. No. 1.8e-05;
0; Mismatches 31;
  Molecules
and Other Molecules Associated With
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APPLICANT: Kovalii, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION UNMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 142853
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US-10-425-115-142853/c
US-10-625-115-142853/c
; Sequence 142853, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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ORGANISM: Zea mays
FEATURE:
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702
                                   910 AGCCCTA 916
                                                                                                          850 AATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAGACT
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                                                                               AATTAGTTAATTTTCTCTTAGAAAAATAAAAATGTCTTGGAAAAATAGAGTTACCAAATT
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ACCCCTA 696
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Pred. No. 2.3e-05;
0; Mismatches 27;
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Pred. No. 2.1e-05;
0; Mismatches 27;
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RESULT 15 US-10-425-114-31957 ; Sequence 31957, Application US/10425114

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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Scoeen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION UNWESER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31957
LENGTH: 2537
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73238H12_FLI
US-10-425-114-31957
Search completed: September 15, 2005, 20:45:31 Job time: 909.859 secs
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                                                                                                 1918
                                                                                                                                                                                         1858 TTAGTTCATTTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTAG 1917
                                                                                                                                                                                                                                                                                        1799 TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAAA 1857
                                                                                                                                             912 СССТАБЛАТБТТТТСССЛАТАЛА 934
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Minimum DB
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Maximum Match 100%
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Perfect score:
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CC252571 OG4BB05TC
CL235046 ZMMBBD057
CG414922 ZMMBBD029
CC439901 PUHRV15TB
CG414927 PUHCV67TB
CC400575 PUHLU61TB
CC400574 PUHLU61TB
CC400574 PUHLU61TB
CC400574 PUHLU61TB
CC630219 OGUCG53TV
CC630219 OGUCG53TV
CC630219 OGUCG53TV
CC630210 OGUCG53TH
CC433618 PUHHP17TD
AL175696 Tetraodon
BZB16381 PUFBA86TD
CC997678 ZMMBH601
CC9333914 OG0AD14TH
CG3333914 OGOAD14TH
CG3333929 OGOAD14TV
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CC385881	CG254365	CG246849	CC676387	BZ996930	AL078714	CG221693	CC385762	CL984151	CL996481	CC003943	BZ676889	CG071791	BZ778636	CC613918	CC620594	BZ784278	CC435780	CG102092	CC430754	82/9/9/6
PUHMJ82TI	OGWFU41TH	OGWAL22TH	OGKAS81TH	PUGIR50TB	Drosophi	OGWMG04TH	PUHFK14TI	ZMMBHd000	ZMMBHf000	PUDJN65TI	PUBIG17TI	PUJBK02TB	ih02f10.g	OGJAG88TV	OGUCC26TV	PUFHV09TD	PUHSN02TI	PUFYW94TI	PUHEPOSTB	FURBA SET

ALIGNMENTS

SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CC656933 LOCUS ð 밁 ORIGIN FEATURES COMMENT REFERENCE DEFINITION Query Match Best Local Similarity Matches 963; Conserv AUTHORS source 404 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACC Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 963) 1 (bases 1 to 963) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics OGWDQ20TM ZM 0.7_1.5_KB genomic survey sequence. CC656933 CC656933.1 GI:32060225 Fax: 301-838-0208 Email: whitelaw@tigr.org Unpublished (2002) Other_GSSs: OGWDQ20TV Class: sheared ends. Seq primer: TR 9712 Medical Center Drive, Contact: Cathy Whitelaw Zea mays CC656933 Tel: 301-838-5843 Conservative /clone="ZMMBMa0554D15" /clone_lib="ZM_0.7_1.5_KB" /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 methylation filtered genomic_DNA library" /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" Location/Qualifiers db_xref="taxon:4577" . 963 68.3%; 0; Score 952; DB 9; Pred. No. 3.8e-191; Zea Mismatches Rockville, mays ď genomic clone ZMMBMa0554D15, DNA ð Length 963; 20850, Indels linear USA GSS 19-JUN-2003 ۲. 8 Gaps 60 463

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RESULT 2
CG224225
LOCUS
DEFINITION
 ACCESSION
VERSION
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1 (bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: GG1AGG88TH

Contact: Cathy Whitelaw
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCAGGTTCGGCAGCTCTCGTGTC
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMM9Ma0716B15"
/clone="ZMM9Ma0716B15"
/clone_1ib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 687)
Whitelaw (C.A., Quackenbush J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Cltek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWDQ20TM
Ocher GSSs: OGWDQ20TM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cathy Whitelaw
                                                                                                                                                                                               Similarity
                GAAAAATAGAGTGCCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTG
                                                                                                                                        GAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTG
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/clone=11b="ZM 0.7_1.5_KB"
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methylation filtered genomic DNA library"
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/strain="B73"
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Pred. No. 1.2e-95;
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                    Seq primer: TF
Class: sheared ends.
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1 (bases 1 to 715)
                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD Tel: 301-838-5843
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                                                                                           h 6.9%;
Similarity 80.1%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
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 TCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCACGAGACGTATCGGG
                               TCACACACCCGCTCTTGTGCCTTTCTTGGATGTCGGCGGTTCCCGTCTGATCGAGGCCCA
                                                   TCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCATCTGACCGAGGCCCA 194
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                                                                                                                                                                      /clone="ZMMBMa0809B10"
/clone=1bb="ZM 0.7_1.5KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                       /mol_type="genomic
/strain="B73"
                                                                                                                                                                                                                                        db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                       organism="Zea mays"
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                                                                                           Score 96; DB:
Pred. No. 8.4e
0; Mismatches
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PUILO19TB ZM 0.6 1.0 KB Z
genomic survey sequence.
CG048704
CG048704.1 GI:33920884
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 Frelinghuysen Road, Piscataway,
Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CL235046 967 bp DNA ZMMBBb0575001r ZMMBBb (HindIII) Zea mays g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
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1 (bases 1 to 967)
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                                                                                                                                                                                                                                                                                                                                                                                                         /clone="ZMMBBb0575001"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/cultivar="B73"
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78.6%;
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Pred. No. 6e-09;
0; Mismatches
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153; Conserv
                     Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
Spermatophyta; Madropogoneae; Zea.
 Yu, Y.,
                                                                                                               GSS
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CG414922
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1 (bases 1 to 814)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                 clade; Panicoideae; Andropogoneae;
1 (bases 1 to 754)
                                                                                                                                                                          ZMMBBb0290L09.r ZMMBBb Zea mays genomic clone ZMMBBb0290L09 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUIL019TD
                                                                                              Zea mays
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Class: sheared ends.
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 Kim, H.R.,
                                                                                                                                                                                                                                                                                                    955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="ZMMBTa0611C13"
/clone lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; &
CoT selected genomic DNA li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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                                                                                                                             GI:34505144
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    selected genomic DNA library"
                                                                                                                                                         sequence.
   Hatfield, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88; DB Pred. No. 4.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.
                                                                                                                                                                                        754 bp
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   Soderlund, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2e-08;
ches 90;
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   Bharti, A.K.,
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 Messing, J
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BACKWARD: M13r
Plate: 0290 row: L
Seg primer: M13r
Class: BAC ends.
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CC439901 CC439901.1 GI:30940477
GSS.
                                                                                  Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHRV15TD
                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                       Contact: Cathy Whitelaw
                                                                                                                                         Whitelaw, C.A., Quackenbush, J., Resnick, A., Fraser, C.M., Yuan,
                                                                                                                                                                    clade; Panicoldeae; Andropogoneae;
1 (bases 1 to 950)
                                                                                                                                                                                                                                  Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of the maize genome Unpublished (2003)
                                                                                                                               Bennetzen, J
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301-838-0208
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ilarity 71.2%;
Conservative
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520 621 9288
                                           Medical Center Drive,
whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="ZMMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/clone="ZMMBBb0290L09"
/lab_host="DH10B"
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/cultivar="B73"
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Pred. No. 4.6e-08;
); Mismatches 47
                                                                                                                                           Yuan, Y.,
                                           Rockville,
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ZMMBTa519D06,
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                                                                                                                                                                                                        Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                         Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHOC67TD
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 652)
Whitelaw, C.A., Quackenbush, J.,
Resnick, A., Fraser, C.M., Yuan,
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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PUHOC67TB ZM_0.6_1.0_KB
genomic survey sequence.
CC384247
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Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                            Bennetzen, J.
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                                                                                        /organism="Zea mays"
/mol_type="genomic D
/strain="B73"
          /clone="ZMMBTa495L13"
/clone=1ib="ZM 0.6_1.0 KB"
/note="Vector: pCR4_TOPO; Site_1:
/note="Vector genomic DNA library"
                                                                                                                                               1. .652
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/clone="lib="ZM 0.6_1.0 KB"
/clone="Vector: pCR4-TOPO; Site_1:
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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                                                                              db_xref="taxon:4577"
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/strain="B73"
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Pred. No. 7.6e-08;
0; Mismatches 47;
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Y., San Miguel,P., Ma,J. and
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                             EcoRI; 0.6-1.0 kb high
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Query Match Best Local Similarity

6.2%;

Score 86.6; DB 8; Pred. No. 8.2e-08;

Length

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Zea mays
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Tel:
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1 (bases 1 to 797)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

"---ink a Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Other_GSSs: PUHLU61TB
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize Genomics Consortium
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                                                                     TTGATTTTTTCAAAA-AAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAA
                                                    TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
                                                                                                                   TTTÄGAGGACGTTGGTAGAGATGGAAAGÁTATAGAGAAAATAATCTTTTAGAGAATGTTA 518
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/clone="nMMBTa480101"
/clone_lib="ZM_0.6_1.0 KB"
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
/not selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="B73"
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                                                                                                                                                                                                                                                                                                                    163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHLU61TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUHLU61TB ZM_0.6_1.0_KB genomic survey sequence. CC400574
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitelaw, C.A., Quackenbush, J., Resnick, A., Fraser, C.M., Yuan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cathy Whitelaw
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                                                   AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCGATAAATCCCCTATCTCATTCTCT
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larity 59.7%;
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/clone=1b="ZM 0.6.1.0 KB"
/clone=Tyector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
/note="Vector: pCR4-TOPO; Site_1" EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Class: sheared ends.
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Other_GSSs: PUJBE19TD
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(bases 1 to 471)

Whitelaw.C.A., Quackenbush.J., Van Aken.S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                     PUFQX12TD ZM_0.6_1.0_KB Zea maye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bennetzen, J.
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PUJBE19TB ZM_0.6_1.0_KB
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COT selected genomic DNA library"
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/strain="B73"
/db_xref="taxon:4577"
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Pred. No. 1.5e-07;
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CC630219/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey (CC630219
CC630219.1 GI:
                                                                                                                                                                                                                                Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUCG53TH
                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 781)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
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Other_GSSs: PUFQX12TB
Contact: Cathy Whitelaw
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                               Seq primer: TF
Class: sheared ends.
                                                                                                        Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
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Fax: 301-838-0208
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                                                                                Email: whitelaw@tigr.org
                                                                                                                                                            9712 Medical Center Drive,
                                                                                                                                                                                                             Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAATTAGTTTATTTCTCTTGAGAAAATATAAAATCACTTGAGAAAATATAGTTTCCAA
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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/strain="B73"
/db_xref="taxon:4577"
          Location/Qualifiers
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Pred. No. 1.6e-07
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906

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SOURCE
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LOCUS
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                                 Query Match
Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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787 ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAA 846
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OG0F183TH ZM_0.7_1.5_KB:
genomic survey sequence.
CG349565
CG349565.1 GI:34266831
GSS.
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Zea mays
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                                                                                                                                                                                                                                                                               Class: sheared ends.
Location/Qualifiers
1. .815
                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
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methylation filtered genomic_DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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                                    Score 85.2; DB 9;
Pred. No. 1.6e-07;
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Search completed: September 16, 2005, 08:08:17 Job time : 4355.69 secs

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ALIGNMENTS

VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION ACCESSION RESULT 1 AX224402 S 밁 S 밁 밁 á ORIGIN FEATURES REFERENCE AUTHORS TITLE JOURNAL Query Match 100.0%; Score 157; DB 6; Best Local Similarity 100.0%; Pred. No. 1.8e-40; Matches 157; Conservative 0; Mismatches 0; source 135 121 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157 61 AAGCCTTTGCCTATTCTGAACCAAGAGGGATACCTACTCCCAAACAATCCATCTTACTCATG 15 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC Zea mays Zea mays Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L. Male tissue-preferred regulatory region and method of using same Patent: WO 0160997-A 9 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. AX224402 255 bp Sequence 9 from Patent WO0160997. AX224402 AX224402.1 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 171 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" . .255 GI:15554644 DNA Length 255; Indels linear PAT 10-SEP-2001 <u>,,</u> 120 74

RESULT 2

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Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Location/Qualifiers
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/mol_type="unassigned
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mes 157; Conserv
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PD 30-OCT-2001
PP 30-OCT-2001
PP 19-JUN-1998 JP 199504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFMAN, PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC ,CO7K14/34,C12Q1/68, PC A01H5/00
CC Strandedness: Single; CC Topology: Linear; FH Key Linear; Location/Qualifiers.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1394)
                                                   Homo sapiens
                                                                                      BD062177.1 GI:22607782 JP 2001520523-A/2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A.
Kendall,T.L.
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                                                                      Homo sapiens (human)
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tissue-preferred regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.9e-40;
Mismatches 0;
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                                                                                                                                                                      Direct Submission
Submitted (13-MAR-2001) Trait and Technology Development, Pioneer
Hi-Bred Intl. 1nc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,
IA 50131-1004, USA
Location/Qualifiers
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AF360356
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                           Fox, T.W., Trimnell, Cloning of Ms45, a
                                                                                                                                                                                                                                                                                                                        Fox, T.W., Trimnell, M.R.
                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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/mol_type="genomic DNA"
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join(<1392. .1768,1898. .2182,2280.
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/cultivar="B73"
                                                                     /db_xref="taxon:4577"
/chromosome="9L"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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/db_xref="taxon:4577"
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DYRPVEHELAFYGEVHGSWFRONASRLRFRGELFYCEVGFESIEFDLQGGFPYAGLA
DGRVVEHELAFYGEVHGSWFRONASRLRFRGELFYCEVGFESIEFDLGGEFPYAGLA
DGRVVRMMGEBAGWEFFA LVANDPDWSEBVCANGVNSTTEXQHEXEBFCGRFCHLGLRFRGE
TGELYVADAYYGLMVVGQSGGVASSVAREADGDPIRFANDLDVHRNGSVFFTDTSMRY
SKXDHLNILLEGEGTCRLLRYDPETSGVHVVLKGLVFFNGVQISGDHQFLLFSETTNC
RIMKYWLEGFRAGEFUBFAALLGFEDDNYRSNGRGQFFWALDCCRTPAQBVFAKEPURC
RIMKYWLEGFRAGEFUBFAALLGFEDDNYRSNGRGQFFWALDCCRTPAQBVFAKEPURC
RIMKYWLEGFRAGEFUBFAALLGFEDDNYRSNGRGQFFWALDCCRTPAQBVFAKEPURC
RIMKYWLEGFRAGEFUBFAALLGFEDDNYRSNGRGGFWVEVLEDRGHEVMKLVSEVREVGRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/product="male fertility protein"
join(1392. .1768,1898. .2182,2280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LWIGTVAHNHIATIPYPLED"
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/codon_start=1
/product="male fertility protein"
/protein_id="AAK2489.1"
/db_xref="GI:14028757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
                                                                                                                                                                                                                                                                        93.0%;
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Patent WO0160997.
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                                                                                                                                                                                                                                                                      Score 146; DB 6;
Pred. No. 7.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 157; DB 8;
Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                     Mismatches
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GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 158

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                        Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality =30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32874 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Areas 6957-70761, 89835-9016, 98951-99009, when the subclone is transposons in the stranded single subclone. Areas 6957-70761, 89835-9016, 98951-99009, when the subclone is transposons in the subclone is transposons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-OCT-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA 3 (bases 1 to 137327) Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J., Collura,K. and Thompson,S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 137327)
                                                                                                                                                                                                                                                                                                                                                          nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-APR-2003) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA On Jan 11, 2003 this sequence version replaced gi:24635891.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-NOV-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA
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AC135206.3 GI:27596977
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Collura, K. and Thompson, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       105316-105607, and 133052-133152 are covered by Monsanto only.
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/note="unknown protein" complement(join(638. .838,1141. .1276,3132. .3244,3326. .342 3513. .3727,3812. .3934,4024. .4054,4157. .4216,5088. .5243,
                                                                                                                        /note="(japonica cultivar-group)"
complement(638. .9495)
                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
|mol_type="genomic DNA"
                                                                                            gene="0J1041F02.1"
                                                                                                                                                                                      clone="0J1041F02"
                                                                                                                                                                                                                  db_xref="taxon:39947"
chromosome="3"
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gene

Sg

translation="MGPPAAPPSPSSSSGGSSRRRRLERRNAAKHIGYDASNFCAYP

gene

CDS

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repeat_region
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TARRICIWECDGEAGDITCDIVAAPLARSCSAKAMPPPAPLFRWMTPPPPRFQRGDGE
EARRGGEAIRKGHRSYSLMLMIQUGISYSVGKSSALPFQKLDASDFDPEKWATRFPP
EGSKFTTPPHHSVDFRWKDYCPAVFRHLRKLFGVDPAEYMLAICGNDTLRELASDGKSG
SCFFITQDDRFMIKTVKKSEVKVLIRMLRSYYEHVRQYKSTILTRFYGTHCIKQAGCP
KIHRRFDLKGSSHGRIDKTERKIDETTTLKDLDLQYAFRLQRFWYEELMKQIQMDCT
FLETQGIMDYSLLGVHFRNDYSVSKIGISQHIAFPKSTGKRKSFEGGSSCELCFVE
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                                                                                                                                     /note="unknown protein"

complement (join (26563. .26772,27082. .27288,27430. .2753

27881. .27940,28051. .28126,28327. .28484,28616. .28678,

28790. .28874,29560. .30575))

/gene="OJ1041F02.4"
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MGENILFYLDPLMCRLVMSLQSSPRILGETCNSAIGST
GEMULTNUBDLCARRAFIEVGI VANAVGRARMETILPPEIBAAIGGFULDYSBLEZ
THGFPSNVAEILDDSFAQYLPHVVPLAFSSCNLDDGSAVDIDDADSVDNGFSGVSSDD
DVNDBFRVRNLSWLTI LADLIFAIRALFASSCNLDDGSAVDIDDADSVDNGFSGVSSDD
EXUVAQACTSLADIVROCGFAILFYLTIRLAADVLKOKDILDTVMNIYIKTMREDDD
KEVVAQACTSLADIVROCGFAILFYLTRLADATLILLROKSCCQVESBOEDDGDID
BDEVLMDAVSDLLPAFAKVMGSYFDPIFTKLFDSLMKFAKSPHPPQDKTMVVATLAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MAQSLELLLIQFLMPDNDARRQAEEQIRRLARDPQVVPALVHHI

/TRAKTPNYQLAAVLLRKKITSHWPKLPPHAKASLKQALIDSITIDHSHLYRRASANV

VSIIAKYAVPAGEWPELLPFITQCSQSPQEDHERVALILFSSLTETIGTTEGSHLNDL

QPILLKCLQDEASSRVRIAALKAVGSFIEYVNDGGDVVKIFRDFVPSILNVSRQCLAN

GEEDVASIAFEIDELLESPAPLLGDSVRSIVQFSLEWCSNQELEININQALIQISW

LVKFKASFLKKKLVIFILQWCFLLTETADEDGDSDLAADRSAAEVLIDMAINLFH

VFPPVLEFASVSFRHINPKYREAAVTSLGVVSEGCCEHLKDKLEDCLKVVLEALKDQE
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GLHRLFADSEPDDAVRDNAAGAIARMIMVQPQSIPLNQILPLVPDVINAFAQVVVSPN
ESDEVKTVVAKAVSHLISVYGQQMQPILSALPPAHANALASFANRR"
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7548. .7593,7679. .7815,8196. .8328,9221. .9495))
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/codon_start=1
                                                                                                                                                                                                                                                                                         /gene="0J1041F02.4"
/note="unber-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGYVPQEEVAIYQSKGAQMRKSGPDVPPGYDPALDAKPKTKAAKRNERRKEKRQQAS
TTNDKGKGLHIEDDAGETDNPKDAVDSVTKQISGIAISESLVVATSSTDATDNSKSES
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/db_xref="GI:29893592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein"
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/gene="OJ1041F02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73982 ...14130,14224. .14354,14459. .14558,15197. .15503)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="unknown protein"
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/db_xref="GI:29893591"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="0J1041F02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="putative transposon,
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join(12372. .12757,12858.
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/db_xref="GI:29893590"
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                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MATASDGSGSGGEQRRLLSIPKEGERIIAPTRRPDGTLRKAIRI
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CCTCCATGCA 119430
                                                             CTTCCATGCA 133
                                                                                                                          CCTTGGCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACGCTGACTCATGCAA 119440
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WSNKWLIADKSPLGTSTTEQNSAEMADGKHLANFHDKOKKSKESGDVIDVDDECLL
ASSCCHASLESKOHERVORBLPEVTPKGCQTANLWTDKYRETAAQVCGNSKIVKF
LNEWLKGWDERGHRNKQNIVTNOSMNGRSCQDGSDTDYSEDASDYENVLLITGPVGCG
KSAAVFACAREQGENVIELNEPKTVVFPFLHKKLLAQTLDLKEDKLHDSSHPSIKYI
FTRVEVHANNANSIISISIAHSSSLSVIKLHCLVNTSDDRANGAYVRQKFEEATKSHGLEK
WSQBEIIGLPISNSLDPASGTPGTAEYKQVINKTLILFEDVDTVPDEDRGFISTILKN
VETTKWPILLTSNKKDPPLPHLLAQLVLDFTVPSAELLSHVDMICKSEGVEITVPQQ
KHIIDAFLGRLNKCLSCPSLLDLDAVHSTVPRIMPDFPCKLSETIYMEIDKTIVTAE
QKKKQMEVSBFEGLELQIMTPLTKGRSAGKTRKKKKKLHGRSADCNDASPCKNDLD
DFHDSPDIPLPSNHQRKRNRRGVVLFAESDDDLADAHAKDAYFTVQEGRLLPQSSEL
PCLYGHGISNIVPBSVFPQOSSVPHLHREVINNQLCFPSESRAFEPASSFQNQLESNM
PGSISQICDTFMSQGISCVPESSFMVGGTSASISSDDLLSSLVSNGLSALRNESTYTA
SVVALEDTNKVENQMTDKPQKCMEDEVGETCBAYVELADRNSVSGALKRVSRVSD
LISESDLMLISCHPFSNDISDSLTPYTESDGFSYSKQLEMGSITYAGHGLCIFLODSQ
ATDDGFVDFLOELLFSGTTTTSLKKFVSSGISCGDGGNISHVKYPSCTSKRERQA
ATDDGFVDFLOELLFSGTTTTSLKKFVSSGISCGDGGGNISHVKYRSTCARFORDA
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PVADWEAHKAGRSSFSSSASTPKPREEPPARDSPVRREVAAEEEPPSLPAPAAPVLP
AKETPRSVAIEAPAPLLRVDPWEPARPDVRKASGEGGIGVREPPVVLKPPESWVRPA
VCVVESTWDILRSFAPEEDSHAHAPASRSGGBAQDAGEEEDDAAAVLTLEELRIGE
TSEEFTGTSSLSTTNDDETSSTTTESKBYJISPWGRFREKIRSWRRGMLLGSGSFGTVF
EGISDEGVFFAVKEVCLCDQGSNAQQCIFQLEQEIALLSQFEHENIVQYYGTDKEDSK
LYIFLELVTQSSLASLYQKYRLRDTHYSAYTRQILNGLTYLHERNIVRDIKCANILV
                                                                                                                                                                                                                                                                                                                                                                                 /note="putative MITE, Castaway-like"
complement(59793. .62196)
/gene="OJ1041F02.6"
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WGPPKAGGGGBAGGAGLPLAAGDGTPBKVKKGRPRKSBAKKPSSNRETTGLEQD
SKDEVILVDBSPQKKGRKGKGKGAALKVPNRKHCKALESTDGHBSCQOLRSSC79A
VLPQKSPTSVDIDLVTGPSEASPVNDNVDALDNEDKPQLIVDLRSEANIAAEENRRLS
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complement(join(35049. 35184, 35866. .36033,36922. .3720;
707280. .38523,40038. .40104,40196. .40287,40406. .40617,
41678. .41760,42229. .42259,42907. .43088,43694. .43753,
44229. .44426,44622. .44676,45877. .45992,46149. .46313,
46447. .46620,47271. .47470,47915. .48019,48200. .48263,
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complement(31668. .31815)
complement(35049. .49855)
/gene="OJ1041F02.5"
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51474. .51836
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YLSSGALSLSAEDIGLLAQCSTFSDRRESETIIEQAIS"
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49589. .49855))
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27679. .27832
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EMLTRQLPYPGLEWTQALYRIGKGEPPAIPNCLSRDARDFISQCVKPNPQDRPSAAKL
LEHPFVNRSMRSIRSMRTSSRSNSSILVLLIMMSWPGRTIRYREAILSTAQSSTPTIA
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85.7%;
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RESULT 11
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TITLE
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Best Local Similarity
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pieces.
BX950854
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                                           BX950854 174806 bp Danio rerio clone CH211-125M22,
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PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huff
Male tissue-preferred regulatory region and
Patent: WO 0160997-A 6 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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AX224399
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                                                                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/db_xref="taxon:4577"
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100.0%; Pred. No. 0.0
cive 0; Mismatches
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100.0%; Pred. No. 2.2e-05;
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of using same
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 172622 bases at least Q40
Consensus quality: 173174 bases at least Q30
Consensus quality: 173177 bases at least Q20
Insert size: 174406; sum-of-contigs
Insert size: 182163; 2.3% error; agarose-fp
Quality coverage: 11.29x in Q20 bases; sum-of-contigs Quality
coverage: 11.03x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Sep 25, 2004 this sequence version replaced gi:42821090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidormes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Danio rerio (zebrafish)
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-125M22"
                                           note="assembly_fragment:00028
                                                                                                /note="assembly_fragment:00366
fragment_chain:1"
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74720: gap of 100 bp
13368: contig of 58648 bp in length
133468: gap of 100 bp
150793: contig of 17325 bp in length
150893: gap of 100 bp
172651: contig of 21758 bp in length
172771: gap of 100 bp
174806: contig of 2055 bp in length
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Homo sapiens BAC clone RP11-525L16 from
AC104134
AC104134.4 GI:19551199
                                                                                                                  Direct Submission
Submitted (20-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Mar 20, 2002 this sequence version replaced gi:18677630.
                                                                                                                                                                                                                                     Direct Submission
Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110127)
Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (04-DEC-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 110127)
Tomlinson,C., Haakenson,W. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-525L16
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 110127)
Waterston, R.H.
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                                                                                                                                                                                                             (bases 1 to 110127)
                                                                                                                                                                                                                                                                                                                   (bases 1 to 110127)
                Contact: sapiens@watson.wustl.edu
Center project name: H_NH0525L16
                                                   Web site: http://genome.wustl.edu/gsc
                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
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Pred. No. 2.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

This sequence was finished as follows unless otherwise noted:

between neighboring data submissions.

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The clone sequenced to the left is RP11-554H10, 2000 bp overlap;
the clone sequenced to the right is RP11-450E9, 2000 bp overlap.
Actual start of this clone is at base position 151996 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5::1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong Rode Coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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1684 1777
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9005. .9219
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/rpt family="Alu"
10124 .10411
                             /note="match to EST BG571642 (NID:g13579295)" 21357 .21652
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20887. .21186
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20737. .20
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.7995. .18056
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|5731. .15824
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4391. .14655
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2314. .12607
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|1362. .11476
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|0483. .10759
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REFERENCE
AUTHORS
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ORGANISM
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AUTHORS
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ACCESSION
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                 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N.,
O'Neil, D., Changagam, U., Peterson, K., Phukhang, P., Pierre, N.,
Pachninka, A., Ramagam, U., Ramagam, C., Roov, P., Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hatez, N., Hatez, N., Hatez, N., Hatez, N., Hatez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Mathews, C., McCarthy, M., Melle, T., Mayor, J., Mencus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Fise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Stojanovic, N., Talamsa, J., Tesfaye, S., Theodore, J., Topham, K., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87753 ACCTCCAAG 87761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 214946)
Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                Research, 320 Charles Street, Cambridge, MA 02141, 3 (bases 1 to 214946)
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AC136896
AC136896.6 GI:29135656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 15, clone RP11-86001
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Pred. No. 3.1;
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RP11-86001, complete sequence.
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     Retta, R., Rise, C., Rogov, P.,
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., Schupback, R., Steman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tayeores, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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----- Project Information
Center project name: L27824
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complement(2941. .3295)
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/rpt_family="LIMC5"
913. .922
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complement (4580. .4711)
                                                                                                 complement (4008.
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                                                                                                                                                                                                                                  /rpt_family="GA-rich" 3601. .4006
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/note="<30 qual SNGL region"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11 Human Male BAC"
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                  family="MIR"
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complement (5336. .5464)
/rpt family="L3"
5935. .641
                                  /rpt_fami
36941. .3
                                                                                                                                32586.
/rpt_family="MIR" complement (38001. .38449) /rpt_family="LIMD1"
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complement(29771.
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/rpt_family="HAL1"
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/rpt_family="HAL1"
complement (25691. .25925)
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22615.
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/rpt_family="L1M1"
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/rpt_family="MLT1E"
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4731. .4751
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complement(4758. .499)
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2585
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                                           .ly="MLT1D"
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                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 13999 bases at least Q40
Consensus quality: 140415 bases at least Q30
Consensus quality: 140735 bases at least Q20
Insert size: 14110; sum-of-contigs
Insert size: 140600; 2.5% error; agarose-fp
Quality coverage: 8.52x in Q20 bases; sum-of-configurations
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                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquirise: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 3, 2004 this sequence version replaced gi:53145936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
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1. (bases 1 to 141810)
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Danio rerio
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Danio rerio clone DKEYP-86C9, *** SEQUENCING IN PROGRESS ***, 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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/rpt_family="MLT1D"
complement(38856. .39656)
    46869:
52415:
52515:
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46769:
19172: contig of 19172 bp in length
19272: gap of 100 bp
46769: contig of 7497 bp in length
46869: gap of 100 bp
52415: contig of 5546 bp in length
52515: gap of 100 bp
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74; Conservative
               McGuire,S.
                          Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 214178)
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                          Danio rerio
                                                                                                      Danio rerio (zebrafish)
                                                                                                                                    BX640577.17
                                                                                                                                                                 complete sequence.
                                                                                                                                                                               Zebrafish DNA sequence from
                                                                                                                                                                                                 BX640577
                                                                                                                                                                                                                                                                                                      CAAACACGCACATATGTTTCC
                                                                                                                                                                                                                                                                                                                                    ACATGGCATACTACATGCTTCGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
                                                                                                                                                                                                                                                                                                                                                             ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment:01302
fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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/db_xref="taxon:7955"
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ragment_chain:1"
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Pred. No. 5.8;
0; Mismatches
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DKEY-117014 in linkage
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Search completed: September 16, Job time: 531.823 secs

2005, 03:01:19

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Best Local
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58421 TCAAAAAAACTTATTAGTCC
                                                                                                                                                                                                                                                    58301
                                                                                                                                                                                  72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                               12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
                                                                                                                                                                                                                                                                                                                                                                                 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquirite: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 8, 2004 this sequence version replaced gi:49659408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-117014
is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Wellcome Trust Sanger Institute
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                                                        CAAACACGCACATATGTTTCC
                                                                                                                                                                                                                                                    ACAGTGACCCCTACATCCTTGTGCCTCAATGCATATTGTACAAGTGTACAGAGGTTGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
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/db xref="taxon:7955"
/clone="DKEY-117014"
/clone_lib="DanioKey"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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52.5%;
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Pred. No. 5.9;
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Perfect score:
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157
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ADB08983 ADB12064_07 AAH76335	AAF22279 ADA02717 ADB72455 ADB95965 ADB959076 ADA51436	AAH76340 AAX07408 AAX07409 AAH76332 AAH76334 AAH76336 AAH76337 AAH76337 AAH76337 AAH76337 AAH76337	SUMMARIES
Adb08983 Alloiococ Continuation (8 of Aah76335 Z. mays M	Aaf22279 BAC conta Ada02717 Mouse Nfa Adb72455 Mouse Nfa Ade95965 Mouse Nfa Ade95966 Human mit Aaa51436 A. thalla	Aah/6340 Z. mays MAax07408 Zea mays Aax07409 Zea mays Aah76332 Z. mays MAah76333 Z. mays MAah76336 Z. mays MAah76336 Z. mays MAah76337 Z. mays MAAK2131 Mouse ato Aca48402 Prokaryot Abn80329 Human Che	Description

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28.4	28.4	28.4	28.4	28.4	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.8	29.2	29.2	29.4	29.6	29.8	30	30
18.1	18.1	18.1	18.1	18.1	'n	18.2	N	'n	'n	'n	18.2	18.2	18.2	18.2	18.2	18.2	18.3	o	18.6	18.7	18.9	19.0	19.1	19.1
1791	1791	1791	1715	1478	164702	164702	164702	164702	164702	110000	51615	1860	1043	778	778	756	1500	110000	1475	110000	1185	373	396	378
12	12	12	8	ω	10	10	10	œ	œ	13	11	6	10	4	4	13	œ	N	9	ω	10	4	10	10
ADQ84654	ADQ85536	ADQ86652	ABA00762	AAF15843	ADB92108	ADB96917	ADB87934	ADB20845	ACF62730	ABD32806_5	ACN45162	ABN67847	ADD71973	AAS32893	AAS32892	ADS57339	ADA68284	AAT42063_06	AAL62902	AAF22303_2	ADF00796	AAH13328	ADD33404	ADD33403
Adg84654 Human tum		Adg86652 Human tum	Aba00762 PSCR rela	Aaf15843 Human pro	Adb92108 Human MDR	Adb96917 Human MDR	Adb87934 Human UGT	Adb20845 MRP1 base	Acf62730 Cancer ba	Continuation (6 of	Acn45162 Human gen	Abn67847 Streptoco	Add71973 Human uri	Aas32893 Human gen	Aas32892 Human gen	Ads57339 Bacterial	Ada68284 Arabidops	Continuation (7 of	Aal62902 Vernonia	Continuation (3 of	Adf00796 Bacterial	Aah13328 Human cDN	Add33404 Mouse mit	Add33403 Mouse mit

ALIGNMENTS

RESULT 1 AAH76340

AAH76340 standard; DNA; 255 BP.

hybrid seed;

promoter;

ds.

mays Ms45 promoter fragment.

M845; male tissue; regulatory region; transcription; male fertility;

29-OCT-2001 AAH76340;

(first entry)

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WPI; 2001-514772/56.
                                                               Albertsen MC,
                                                                                       13-FEB-2001; 2001WO-US004527
                                                                                              23-AUG-2001.
                                                                                                             Zea mays.
                                                                               15-FEB-2000; 2000US-00504487.
                                                                                                     WO200160997-A2
                                                                       (PION-) PIONEER HI-BRED INT INC.
                                                               FOX TW,
                                                               Garnaat CW,
                                                               Huffman
                                                               ģ
                                                               Kendall TL;
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The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays MS45 promoter fragment

The

of.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

Example 5; Fig 8; 50pp; English.

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RESULT 2
AAXO7408
ID AAXO
AC AAXO
AC AAXO
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CXX Zea
XXX 
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Best Local Similarity
Matches 157; Conserv
                                                                                             Matches
                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                   The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably M845), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
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                                                                                                                                                                                        BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue-preferred regulatory region
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                                                                                          Score 157; DB 2;
Pred. No. 2.1e-42;
; Mismatches 0;
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Pred. No. 1.3e-42;
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                                                                                                                                        Length 1394;
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                                                                                                                                                                                  Query Match
Best Local Sim
Matches 157;
                                                                                                                                                                                                                                                                                         The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin, Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                                                                                                                                                               Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-105628/09.
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                              CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                                                         CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
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CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                           AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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                                                                                                                                                                                     Conservative
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Pred. No. 2.1e-42;
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RESULT 4
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RESULT 5
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Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the M945 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an M845 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.

    mays Ms45 male tissue-preferred regulatory region encoding DNA.

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                                                            29-OCT-2001
                                                                                                                                                                        AAH76333 etandard;
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Pred. No. 2.1e-42;
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                                                                                                                         Z. mays Ms45 male
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                                                                                             Ms45; male tissue;
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                                                                                                                                                                                 AAH76334;
                                                                                                                                                                                                             AAH76334 standard;
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                                                                                  hybrid seed;
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                                                                                                                         tissue-preferred regulatory region fragment.
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                                                                                             regulatory region; transcription;
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Best Local S
Matches 157
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                                                                                                                                                                                      Ms45; male tissue;
                                                                                                                                                                                                            mays Ms45 male tissue-preferred regulatory region fragment.
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 Albertsen
                        (PION-) PIONEER HI-BRED
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Pred. No. 5.4e-39;
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The
                                                                                                                                                 A male tissue-preferred regulatory region comprising essential for initiating transcription of the MS45 mediating fertility in a male plant.
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                                                                                                                        Claim 14; Page
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                                                                                                                                                                       The invention relates to detecting atopic dermatitis or psoriasis comprising assaying the levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis, comparing these levels with those of a healthy person, and determining that if the levels of indicators are higher or lower, then this indicates the disease. Also included are a reagent for detecting atopic dermatitis or psoriasis, a kit for screening for treatments, a transgenic non human vertebrate animal models for the diseases, an agent for inducing the diseases in mice and a DNA chip for assaying for the indicator genes. The method is used for treatment, detection and animal models for research of atopic dermatitis and psoriasis. The present sequence is a Mouse atopic-dermatitis/ psoriasis-associated EST
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Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting atopic dermatitis or psoriasis comprises expression of an indicator gene at a rash site and person with atopic dermatitis or psoriasis.
                                                                                                                    Sequence 3267
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miteuishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-2002; 2002JP-00229319
14-MAY-2003; 2003JP-00136544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2003; 2003WO-JP009999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-inflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK52131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADKS2131 standard; cDNA; 3267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOX RES INC. (UYJU-) UNIV JUNTENDO.
                                                                                                                                                             (expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                                      66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a DNA fragment upstream of the TATA box of a M845 male-tissue preferred regulatory region nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogawa K,
11 K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 164; 484pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                             sequence tag).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST; atopic dermatitis; psoriasis; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 14
                                        Conservative
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                                                                                                                  BP; 1029 A; 658 C; 590 G; 990 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antipsoriatic; rash; expressed sequence tag
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                                                     20.6%;
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Pred. No.
                                                         Score 32.4;
Pred. No. 2
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                                      Mismatches
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                                                                          DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogawa
                                      56;
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                                      Indels
                                                                          Length
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RESULT 10
ACA48402/c
ID ACA484
The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibited by the cativity of a gene in an operon required for proliferation or the activity of a gene in an operon required for capaliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of which each of the strains is present in a culture confirmation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-00815242

06-SEP-2001; 2001US-00948993

25-OCT-2001; 2001US-00342923P

08-FEB-2002; 2002US-00072851

06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; SEQ ID NO 36272; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug design;
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GT 2895
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Carr G
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Forsyth
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Xu HH;
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RESULT 11
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ID ABN803
XX ABN803
XX ABN803
XX 15-JUL
XX Human;
KW Human;
KW Heart
KW dwarfi
KW Gwarfi
KW Gwarfi
XX 2002
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Matches 55
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (I of genes associated with development selected from 87 genes listed in specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with
                                                                                                                                                                                                                                                                                                         Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a of a segment of chemically pretreated DNA of genes associated w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart disease; epilepsy; histone deacetylation; dwarfism; single nucleotide polymorphism; SNP; c
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                      The present invention relates to a recombinant DNA construct of a plar (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for construction of transgenic plant and animal cells expressing selected
                                                                                                                                                                                                             Recombinant DNA construct comprising a plant centromere, useful producing stably inherited michrosomes which can serve as vector construction of transgenic plant and animal cells.
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18-MAY-1999;
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17-SEP-1999;
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CC The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (AAA01482-ADA03094), and to CC carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC Anucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof: The sequences of the invention were identified using CC art random. Many of these do not carry transduced host oncogens or CC gathogenic trans-acting viral genes, meaning that cancer incidence is a CC great consequence of the effects of proviral integration into host CC pathogenic trans-acting viral genes, meaning that cancer incidence is a CC great consequence of the effects of proviral integration into host CC pathogenic transest cancer, prostate cancer incidence is a CC gene. The CA nucleic acid sequences can be used to diagnose CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular CC tissues. (An uncleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The CC present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this cCC in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAAATCCCAAACCCTAAATCTAATTCCTTAAC 7209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18698 A; 13554 C; 13083 G;
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Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein,
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                                                                                     carcinomas, e.g. lymphomas, cancers, usuprasm, amouse gene of the invention. sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                         The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully define in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                                                                                                    02-MAR-2001; 2001US-00798586
23-OCT 2001]; 2001US-00004113
08-NOV-2001; 2001US-00052482
30-NOV-2001; 2001US-00997722
20-DEC-2001; 2001US-00034650
                                                                         Sequence 79467
                                                                                                                                                                                                 Claim 1; SEQ ID NO 283; 2304pp; English.
                                                                                                                                                                                                                          cancers, neoplasm, adenocarcinoma, or sarcomas
                                                                                                                                                                                                                                    New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2001; 2001WO-US051291
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neoplasm; adeno
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                                                                         BP;
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adenocarcinoma; sarcoma; gene.
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel recombinant nucleic acids for use in diagnosis and treatment of cancer, especially carcinomas, as well as the use of compositions in screening methods. The compositions of the invention may have cytostatic activity whilst the disclosed sequences may be useful for gene therapy. The carcinoma associated nucleic acids and proteins are useful for diagnosing and treating carcinomas, for screening lymphoma, breast cancer, prostate cancer or leukaemia, or for screening drug candidates or bioactive agents capable of binding to, or modulating the activity of, a carcinoma associated protein. The present sequence is the genomic DNA sequence of the mouse Nfatcl gene which is a carcinoma associated gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New carcinoma associated nucleic acids and proteins, useful for screening drug candidates, or for diagnosing and treating carcinomas, e.g. lymphoma, breast cancer, prostate cancer or leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy;
lymphoma; breast cancer; prostate cancer; leukaemia; ds; mouse; murine;
Nfatcl.
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
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CACACACACACACACACACACACACACAAGCTTGTGGCTC 53879
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| Com2 6/ptodata/1/ina/5A_COMB.seq:*
| Com2 6/ptodata/1/ina/5B_COMB.seq:*
| Com2 6/ptodata/1/ina/6B_COMB.seq:*
| Com2 6/ptodata/1/ina/6B_COMB.seq:*
| Com2 6/ptodata/1/ina/6B_COMB.seq:*
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3 US-08-880-499-1
3 US-08-880-499-2
3 US-09-949-016-16073
4 US-09-949-016-14712
4 US-09-949-016-14713
4 US-09-949-016-17474
4 US-09-949-016-17474
4 US-09-949-016-17470
4 US-09-949-016-17470
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5 US-09-949-016-16740
6 US-09-134-001C-1413
6 US-09-134-001C-1413
6 US-09-134-011C-17368
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                          Sequence 1, Appli

Sequence 2, Appli

Sequence 16073, Ap

Sequence 1081, Ap

Sequence 1, Appli

Sequence 14713, A

Sequence 15502, Ap

Sequence 15502, Ap

Sequence 119201,

Sequence 111201,

Sequence 14147, A

Sequence 1413, Ap

Sequence 1413, Ap

Sequence 1413, Ap

Sequence 1413, Ap

Sequence 3747, Ap

Sequence 2556, Appli

Sequence 2556, Ap

Sequence 2568, Appli

Sequence 2568, Appli

Sequence 2703, Appli

Sequence 1703, A

Sequence 1703, A
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US-08-880-499-1
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29 27.2 17.3 62776 4 US-09-949-016-17576 30 27.2 17.3 100848 4 US-09-949-016-17576 31 27.2 17.3 158735 4 US-09-949-016-17189 32 27.2 17.3 158735 4 US-09-949-016-17130 32 27.2 17.3 158735 4 US-09-949-016-17130 33 27 17.2 4780 4 US-09-949-016-12088 35 27 17.2 47030 4 US-09-949-016-13037 36 27 17.2 47030 4 US-09-949-016-15039 37 27 17.2 47030 4 US-09-949-016-15039 38 27 17.2 47030 4 US-09-949-016-15039 39 27 17.2 194537 4 US-09-949-016-12928 40 27 17.2 194537 4 US-09-949-016-12928 41 26.8 17.1 2655 4 US-09-949-016-12740 42 26.8 17.1 3114 3US-08-946-026-9 43 26.8 17.1 156950 4 US-09-949-016-12227 44 26.8 17.1 156950 4 US-09-949-016-12227	ი	ი	n	ი									ი	ဂ	a	ი	a	
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	15946, A	12227, A	12, Appl	9, Appli	8379, Ap	12740, A	12928, A	15040, A	15039, A	13038, A	13037, A	12088, A	678, App	17130, A	11989, A	39, Appl	17576, A	13/13/ 0

ALIGNMENTS

CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave.,
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME NUMBER OF SEQUENCES: 50131 P.O.

; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (ger US-08-880-499-1 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION UNUMBER: 32,733
REGISTRATION UNUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: LENGTH: 1394 base pairs
TYPE: nucleic acid DNA (genomic)

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Query Match 100
Best Local Similarity 100
Matches 157; Conservative 100.0%; Score 157; DB 3; 100.0%; Pred. No. 5.6e-45; rative 0; Mismatches 0; Length 1394; Indels 0 Gaps

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                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
                                                                                                                                                                                                                   Matches 157;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Albert:
APPLICANT: Fox, T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTED: 2

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS INTERNATIONAL, INC.

PROPERSEE: PIONEER HI-BRED INTERNATIONAL, INC.

PROPERSEE: PIONEER HI-BRED INTERNATIONAL, INC.

PROPERSEE: PIONEER HI-BRED INTERNATIONAL, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Johnston
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CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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                                                                                                                                                                                                                                                                                                           linear
E: DNA (genomic)
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Pred. No. 5.6e-45;
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PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FasteEQ for Windows Version 4.0
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; Sequence 1081, Application US/09543681A
; Patent No. 6605709
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(385136)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-16073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-949-016-16073/c
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                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1081
LENGTH: 1185
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APPLICANT: GARY BRETON
                                                                                         Matches
                                                                                                             Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                    TYPE: DNA ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 385136
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940 CAACAATTTGTTTTTGTCCACCAGAAAGACCTAACCCATTTTCTCCCAAGGACATATCTA
                               35 CAACCGTTCGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGGATACCTA 94
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Similarity 57.3%;
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                                                                                    Score 29.6; DE Pred. No. 2.4; 0; Mismatches
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Pred. No. 14;
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RESULT 6
US-09-643-990A-1/c
US-09-643-990A | Sequence 1, Application US/09643990A | Patent No. 6528289 | GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
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US-09-557-884-1/c
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Patent No. 6506581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.6%;
Best Local Similarity 51.5%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-195
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECHONE: 301-309-8504
TELEPHONE: 301-309-8504
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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Pred. No. 66
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US-09-949-016-14712/c
Sequence 14712, Application US/09949016
PATENT NO. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS (
FILE REFERENCE: CL001307
CURRENT APPLICATION UMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-AUG-2000

CLASSIFICATION DATA:

APPLICATION UNMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

APPLICATION UNDBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186F1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                               LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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Hamilton O. Smith
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51.5%; Pred. No. 6
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0; Mismatches
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                                                              ASSOCIATED
OF DETECTION AND
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Sequence 14713, Application US/09949016

| Patent No. 6812339
| GENERAL INFORMATION: Tritle OF INVENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION APPLICATION WITH HUMAN DISEASE, METHODS OF DETECTION APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
US-09-949-016-15502
; Sequence 15502, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; ORGANISM: Human
US-09-949-016-14713
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Best Local S
Matches 45
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 14712
LENGTH: 64190
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Best Local :
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PRIOR FILING DATE: 2000-10-03
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Pred. No. 24;
0; Mismatches
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Pred. No. 24
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                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17447
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                         Query Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 17447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: VENTER, J.
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Fast
SEQ ID NO 15502
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR TILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                   LENGTH: 41815
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                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 CTGAACCA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FastSEQ for Windows Version
                                                                                                          AGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGC 121
                                   AACTTCCATGCAAACACGCACATA 145
                                                                             AGACATGCAGATTCACACACATCCGCATAGCTGCTCCTACGGATCCCTGGTCACTCATTC 33117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTTATTTCATGGTGTTTTTAGGGTTAATGTTGTAGCATCCATTTAGCCTTGTCAAGG 4491
ATGTCACATAGAGACATGCATGTA 33141
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63.2%;
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58.3%;
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                                                                                                                                                                            Score 28; DB 4;
Pred. No. 38;
                                                                                                                                                              Mismatches
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                                                                                                                                                            35;
                                                                                                                                                                                                 Length 41815;
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RESULT 11
US-09-949-016-191201/c
; Sequence 191201, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 00/231,498
PRIOR APP
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US-09-949-016-14149
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/ ORGANISM: Human
US-09-949-016-191201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PACENT NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,766

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 62; Conserv
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SEQ ID NO 14149
LENGTH: 11490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Local Similarity 58.0%;
       5582
                                                                                                                                             5642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                               CCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAA 156
                                                                                                                                     CAGGGCCTCTGCTTCCCTGCCCCTCCCCCTGCCCCCACCTCACCAGGAGGAAGCCCACGC 5583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGCAAATAGGATGGAAATA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGCAACTTCCATGCAAACA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCTGACGTTGCATGCACACRTGCACGCGCGCACAAACACACACACACTCTCTCTCATT 263
CCTTGCACACCTGATGCCACATCCGCTTGAGTGGCAGGCGAGTGAAGATGTTGCCCAAA 5524
                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                            17.7%;
                                                                                                                                                                                                                                                                        Score 27.8; DB Pred. No. 26; 0; Mismatches
                                                                                                                                                                                                                                                                               0,
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Pred. No. 7.9;
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                                                                                                                                                                                                                                                                               57; Indels
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                                                                                                                                                                                                                                                                                                                                            Length 11490;
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CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1813
LENGTH: 1413
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
PEATURE: PATENTIN VER. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-710-279-1813/c
; Sequence 1813, Application US/09710279
; Patent No. 6703492
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US-09-949-016-16740
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SEQ ID NO 16740
LENGTH: 14952
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                                                                                                                                                                            Matches
                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CCURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                   1213 ATTGAATTCTACGTGCTCGTTCCACAGTTTGTTTATCTTCATCTGATAATTCATCCATAC 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 GGTTTTACACACACACACA 148
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                                                                                                                           14 AIGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTAT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 TGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACCAATCCATCTTACTCATGCAACCTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                     74 TCTGAACCAAGAGGATACCTACTCCCAAACAAT 106
                                                                                                                                                                         52;
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CAAGAATCGCAATAATATCTTGTAACTCTCTAT 1121
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59.5%;
                                                                                                                                                                                          17.5%; Score 27.4; 55.9%; Pred. No. 15;
                                                                                                                                                                       0; Mismatches
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Pred. No. 29;
0; Mismatches
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                                                                                                                                                                         Indels
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RESULT 13 US-09-949-016-16740

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US-09-134-001C-1413/c

Sequence 1413, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR PRILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NO: 5674

SEQ ID NO 1413

LENGTH: 1428

TYPE: DNA
ORGANISM: Staphylococcus epidermidis

US-09-134-001C-1413
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Search completed: September 15, 2005, 08:25:04 Job time: 31.7481 secs
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                                                                                                                                                74 TCTGAACCAAGAGGATACCTACTCCCAAACAAT 106
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/PCT_NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US07_NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US08_NEW PUB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US08_NEW PUB.seq:*

8: /cgn2 6/ptodata/2/pubpna/US08_NEW PUB.seq:*
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10230.248 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	

0 7 5 5 4 6 5 P	Result No.
157 157 157 146 50 40 32.2	Score
100.0 100.0 100.0 93.0 31.8 25.5	Query Match
255 1394 158 50 40	Query Match Length DB
122222	DB
US-10-713-381-9 US-10-713-381-1 US-10-713-381-2 US-10-713-381-3 US-10-713-381-5 US-10-713-381-6 US-10-713-381-6 US-10-674-124A-9081	ID
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e 53712, e 141945, e 17846,		Sequence 222444, Sequence 222445, Sequence 222444, Sequence 222444, Sequence 222445, Sequence 222445,	e 254612, e 254612, e 254612, ce 179264 ce 179264, A e 2154, A e 11, App ce 1, App ce 1, App ce 1, App	Sequence 36272, A Sequence 1496, Ap Sequence 244811, Sequence 244811, Sequence 223, Appl Sequence 17, Appl Sequence 170626, Sequence 170626, Sequence 170626, Sequence 57018, A

ALIGNMENTS

RESULT 1 US-10-713-381-9

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Sequence 9, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEK, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: KENDALI, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF TITLE OF INVENTION: USING SAME

FILE REFERENCE: 578R
CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: US/10/713,381

CURRENT FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 255
TYPE: DNA

ORGANISM: Zea may8

US-10-713-381-9

Query Match
Best Local Similarity 100.0%; Score 157; DB 20; Length 255;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Sequence 2, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METH
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R

CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION UNUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24
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CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 08/880,499

PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1

LENGTH: 1394
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US-10-713-381-2
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; ORGANISM: Zea mays
US-10-713-381-1
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US-10-713-381-1
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Publication No. US20040221331A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 157; Conserv
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APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
SOFTWARE: PatentIn Ver. 2.0
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RESULT 5 US-10-713-381-5

Sequence 5, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:

APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W. APPLICANT: GARNAAT, CARL W.

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SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 158
TYPE: DNA
ORGANISM: Zea mays
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; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
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Best Local Similarity
Matches 157; Conserv
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Best Local S
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APPLICANT: HUPFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 09/806-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
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GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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ilarity 99.4%;
Conservative
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Pred. No. 8.2e-40;
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158
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US-10-674-124A-9081/c
Sequence 9081, Application US/10674124A
Publication No. US20040197797A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-713-381-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
APPLICANT: INCKO, Hidetoshi
APPLICANT: TAMIYA, Gen
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REFERENCE: ORLN-003CIP
CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/257,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W. APPLICANT: GARNAAT, CARL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, APPLICANT: HUFFMAN, APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
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CURRENT FILING DATE: 2003-11-14
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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 40
TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                           40;
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50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIMMY L.
                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%; Score 40; DB 20; Length 40; 100.0%; Pred. No. 0.0011;
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US-10-282-122A-36272/c; Sequence 36272, Application US/10282122A; Publication No. US20040029129A1
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               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR TILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/296,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
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APPLICANT:
TITLE OF IN
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APPLICANT:
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APPLICANT: Zamudio, Carl
APPLICANT: Malone, Chery
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PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 27110
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PRIOR APPLICATION NUMBER: PCT/JPD0/07621
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: JP2000-112699
PRIOR APPLICATION NUMBER: JP2000-112699
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence: 250186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Located on chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: chr5.fa.O7frz.139538206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 ATTTTGAAGAAAACAGTGGGCCACCCTCAAAAAAACCCCAAACTACTCATCTAACTTAAAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 CAAACACGCACATATGTTTCCTGAA 156
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                                                                                                                                                                                                                                                                                                                                               Yamamoto, R
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                    קלה,
Grant
הירח, Robert
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Pred. No. 1.3;
0; Mismatches
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RESULT 10
US-10-027-632-244811
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_101357C.
US-10-437-963-1496
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; ORGANISM: Streptococcus mutans
US-10-282-122A-36272
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 36272
                                                                                                                                                                                                                     Matches
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Best Local (
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LENGTH: 1122
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APPLICANT:
APPLICANT:
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APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Local Similarity 58.5%;
les 55; Conservative
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                                                                                                       120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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                                                                                                                                                                    60 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACCAATCCTTACTCAT 119
                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                      Similarity
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Wu, Wei
Boukharov, Andrey A
Barbazuk, Brad
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                                                                     TCAGATCCACAAATCGCACCCTCCCATATCTGCTGAAC 216
                                                                                                                                             AATTTCAGCAAAAGAACGTTCAATTTTTTCCTGA 141
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                    Score 30.8; DB 19; Pred. No. 5.6;
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Sequence 244811, Application US/10027632

| Sequence 244811, Application US/20030204075A9
| GENERAL INFORMATION: APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
| CURRENT APPLICATION NUMBER: US/10/027,632
| CURRENT FILING DATE: 2002-04-30
| PRIOR APPLICATION NUMBER: US 60/218,006
| PRIOR APPLICATION NUMBER: US 60/198,676
| PRIOR APPLICATION NUMBER: US 60/198,676
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/195,218
| PRIOR APPLICATION NUMBER: US 60/185,218
| PRIOR APPLICATION NUMBER: US 60/185,358
| PRIOR APPLICATION NUMBER: US 60/167,363
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US-10-027-632-244811
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PRIOR FILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR FILLING DATE: 1999-11-23
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LENGTH: 559
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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US20020198371A1
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APPLICANT: Engelhard, Eric
APPLICANT: MOTTIB, DAVId
ITILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/ENS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 241
SOFTWARE: Patentin version 3.1
SEQ ID NO 223
LENGTH: 79467
TYPE: DNA
CDEANTEM: Miss misscrilis
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US-10-052-482-223
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; ORGANISM: Human
US-10-027-632-244811
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Best Local
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SOFTWARE: FRETSEQ for Windows
SEQ ID NO 244811
LENGTH: 559
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LOCATION: (20762)..(20781)
OTHER INFORMATION: "n" at
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NAME/KEY: misc_feature
LOCATION: (10089)..(10620)
OTHER INFORMATION: "n" at
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LOCATION: (4099)..(4369)
OTHER INFORMATION: "n" at positions 4099 to 4369 can be any base
                                               NAME/KEY: misc feature
LOCATION: (30751)..(30916)
OTHER INFORMATION: "n" at
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LOCATION: (13273)..(13370)
OTHER INFORMATION: "n" at
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OTHER INFORMATION: "n" at positions
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NAME/KEY: misc_feature
LOCATION: (46579)..(46772)
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NAME/KEY: misc feature
LOCATION: 11187, 11188, 11189, 11190, 111
LOCATION: 11196, 11197, 11198, 11199, 11
LOCATION: 11214, 11205, 11206, 11207, 11
LOCATION: 11212, 11213, 11214, 11215, 11
LOCATION: 11210, 11213, 11214, 11215, 11
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Matches
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SEQ ID NO 11
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APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL
FILE REFERENCE: RTS-0478
                                                                                                                                                                                                                                                                                                                                                    PRATURE:
NAME/KEY: misc_feature
LOCATION: 11154, 11155, 11156, 11157, 11158,
LOCATION: 11163, 11164, 11165, 11166, 11167,
LOCATION: 11171, 11172, 11173, 11174, 11175,
LOCATION: 11179, 11180, 11181, 11182, 11183,
LOCATION: 1179, 11180, 11181, 11182, 11183,
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CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 11220
OTHER INFORMATION: n = A,T,C
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NAME/KEY: misc feature
LOCATION: 11127, 11122, 11123, 11124, 11125,
LOCATION: 11130, 11131, 11132, 11133, 11134,
LOCATION: 11138, 11139, 11140, 11141, 11142,
LOCATION: 11146, 11147, 11148, 11149, 11150,
OTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: H. sapiens
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LOCATION: (77382)..(770
OTHER INFORMATION: "n"
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les 57; Conserv
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                                                                                                                 Similarity
                                  TTTCTTTTTCTAAAACTGAAATTCCATGAAAAAAGGAATATCAATTTTAAAACTACCCA
                                                               TTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCA 109
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                                                                                                  Conservative
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Pred. No. 31;
0; Mismatches
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Pred. No. 31;
0; Mismatches
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11208,
11216,
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11168,
11176,
11184,
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RESULT 14

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CURRENT APPLICATION NUMBER: US/10/713,381
; CCURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-713-381-4
; Sequence 4, Application US/10713381
; Publication No. US20040221331A1
                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 170626

LENGTH: 843

TYPE: DNA

ORGANISM: Human

US-10-027-632-170626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-027-632-170626, Application US/10027632; Sequence 170626, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
          Query Match
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Matches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 578R
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          ch 19.1%;
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69; Conservative
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          Score 30; DB 13; Length 843; Pred. No. 9.5; O; Mismatches 65; Indels
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Search completed: September 15, 2005, 20:45:38 Job time : 108.248 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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9b est1:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AQ376006 RPCI11-16	CA151882 SCJFRZ201	CK001730 AGENCOURT	AQ811019 HS_5382_A	CA495416 AGENCOURT	N25701 yx79e04.sl	BG265863 1000039D0	BG242888 602355872	BH168285 VV_SBa000	BY053139 BY053139	BZ149047 CH230-453	CC480196 CH240_307	BF227024 uz17e08.x	BH752563 SALK_0188	AK028832 Mus muscu	BC048853 Mus muscu	AL322183 Tetraodon	BF682258 602117694	AL055406 Drosophil	BI453933 603174018	BB004373 BB004373

ALIGNMENTS

Qу Db 42	Query Match Best Local Matches 15	source ORIGIN	FEATURES	AUTHORS TITLE JOURNAL COMMENT	RESULT 1 CC656939/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	/ Match 100.0%; Score 157; DB 9; Length 687; Local Similarity 100.0%; Pred. No. 1.8e-39; nes 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1687 /organism="Zea maye" /mol_type="genomic DNA" /strain="873" /db_xref="taxon:4577" /clone="ZMMBMa0554015" /clone=1ib="ZMMBMa0554015" /note="Vector: DBCSK-; Site=1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"	TIGK 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends. Location/Qualifiers	Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002) Other GSSs: OGWDQ20TM Contact: Cathy Whitelaw	CC656939 CC656939 CC656939 GC656939 CC656939.1 GI:32060231 Zea mays Zea mays Zea mays Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea. 1 (Dases 1 to 687)

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RESULT 3
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CG224225.1 GI:34124113
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1 (bases 1 to 915)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OffA008TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
/methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                        100.0%; Score 157; DB 9; 100.0%; Pred. No. 1.9e-39;
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                           DNA linear GSS 19-JT genomic clone ZMMBMa0554D15,
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                                                                                                                                                                        Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                  genomic survey sequence. CE588104
Contact: Kirkness EF
The Institute for Genomic
                            14512627
                                                                                                                                                                                                                      CE588104.1 GI:36904885
                                            22875432
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Class: sheared ends.
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: whitelaw@tigr.org
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/mol_type="genomic D
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Pred. No. 2e-39;
0; Mismatches
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121 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 636)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                  CE588104 1inear GSS 2 Ligr-988-dog-17000366359543 Dog Library Canis familiaris
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGWDQ20TV
The dog genome: survey sequencing and comparative Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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/clone="E2M/BMA0554DL5"
/clone_il="ZM/DMA0554DL5"
/clone_il="ZM_0.7_1.5 KB"
/note="Vector: pBCSK.; Site_1: HincII; 0.7-1.5 methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                                                                                                                                                                                                                                            Waldhoferstrasse 98, D-69123 Heidelberg,
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; 1 (bases 1 to 643) Chlueter, T., Hermanns, J., Weindel, M., Schuette, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Schlueter
                                                                                                                                                                                                                                                                                                                                                                                                        Henrich, J. and Loebbert, R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
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Class: shotgun
                                                                              Similarity
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TATTTTTTCCCAGTTCAAGGCATCCTTGTTTGGACCCAAGGGTATACCTCATTTTTAAAA
                   TCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACA 104
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                                                                                                                                                                                                                                                                                                               Thomas.Schlueter@lionbioscience.com
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                                                                                                                                                                     /db_xref="taxon:9615"
/t1ssue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were
peripheral blood"
                                                                                                                                      /clone_lib="DC
/note="Organ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
                                                                                                                                                                                                                                                 organism="Canis familiaris"
|mol_type="mRNA"
                                                                                                                                                                                                                                     'strain="Beagle"
                                                                                                                                                                                                                                                                                                location/Qualifiers
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58.4%;
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                                                                                                                                      lib="DG11-kidney"
"Organ: kidney; Vector:
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                                                                           Score 37.8;
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R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@sgc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing : TJ
LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Kuniya Ābe (ābe@rtc.rike) Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyaddai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Massahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
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Mus musculus molossinus
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BAC end Sequences of Library MSMg01
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Mus musculus molossinus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                        CAAACTTTTTTTG
                                                                                                                                                                               AAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCA 141
                                                                                                                                                                                                                    CTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACC
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                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus mu/mol_type="genomic DNA"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
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: EcoRI
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                                                                                                                                                                                                                                                                                        Score 37.8; DB Pred. No. 0.46; O; Mismatches
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clone:MSMg01-170B12.TJ,
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                                                                                                                                                                                                                                                                                                                           Length 1085;
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci.P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watsahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Mateuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Togabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
BB505306
BB505306.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library, Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fikuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jul 27, 2000 this sequence version replaced gi:9514268.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues
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Computational Analysis of Full-Length Mouse CDNAs Compared with
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81-45-503-9216
/clone lib="RIKEN full-length enriched, 10 days lactation, adult female mammary gland"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                  /dev_stage="10 days lactation, adult"
/lab_host="DH10B"
                                                                                                                                                                                                          /sex="female"
                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                   organism="Mus musculus"
mol_type="mRNA"
                                                                                                                                                                         tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                 clone="D730002G06"
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1 (bases 1 to 1677)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CL026582 1677 bp DNA CH216-23G24_Sp6.1 CH216 Xenopus tropicalis CH216-23G24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Length: 175000 Std Error: 0.00 Seq primer: Sp6 ATTTAGGTGACACTATAG Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus tropicalis
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/cell line="Stock 248 F7A2, inbred N7"
/clone lib="CH216"
/notee="Vector: pTARBAC2.1; CHORI-216 X/
BAC library"
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/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
                                                                                                                         clone="CH216-23G24"
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Pred. No. 6.8;
                         pTARBAC2.1; CHORI-216 Xenopus tropicalis
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RESULT 9
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nes 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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1 (bases 1 to 440)
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Mammalia; Eutheria; Primates;
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TCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCT
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                                              CTTTGGCCAGCAAACTAGTATATCATÄTTCCTCCCCAAAGCAACACCTCCTACTTATTT
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                                                                            CTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAA 105
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                                                                                                                                                                               /clome_lib="NCI_CGAP_Ov23"
/note="Organ: ovary; Vector: pcMV-SPORT6; Site 1: Sall;
/note="Organ: ovary; Vector: pcMV-SPORT6; Site 1: Sall;
Site 2: Noti; Cloned uniddirectionally. Primer: Oligo dT.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastassis positive. Life
Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                        /tissue_type="tumor, 5 pooled (see description)"
lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                              'organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                  clone="IMAGE: 2218451"
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IMAGE:2218451 3',
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CR575123
CR575123.1
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CR575123
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                                                                                                          GSS.
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Contact: Croning MDR
                                                                                                                       AL064657.1
                                                                                                                                        AL064657
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480 TCTGAATTATGAAAAGGCCATCTCCCATAGACTCCATTTTATGCAAGTAATTTACATTTT
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Drosophila melanogaster
Eukaryota; Metazoa; Archropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                            CNS003FV 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08003 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: THGA024m33.plkbSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
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Croning, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N.
Sanger Xenopus tropicalis EST project 2001 (2004)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                            Drosophila melanogaster (fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
/note="Vector: pCS107; Site_1 : EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tailbud
head. EcoRI-NotI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage="tailbud head (stage 28-30)"
/lab_host="Escherichia coli DH10B."
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/mol_type="mRNA"
/db_xref="reaxon:8864"
/clone="THdA024m23"
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Pred. No. 20;
0; Mismatches
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; Pipidae;
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE690384 347 bp mRNA linear uw66f12.y1 Soares mammary_gland_NMLMG Mus musculus IMAGE:3466991 5', mRNA sequence.
                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE690384.1 GI:10078008
EST
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, 1 (bases 1 to 347)
                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBNWTKDAAYBDKDDATKKBSKYCCMAAVSCCARDDNYWAMCHDKKYCMMCHWWHAHAAA
                                                                                                                                                                                                    primer: -40RP from Gibco
                                                                                                                                             quality sequence stop: 270.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                            organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BACR08003"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
/sex="female (lactating)"
                          clone="IMAGE:3466991"
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21.9%;
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Pred. No. 2:
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SOURCE
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VERSION
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AJ746802/c
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JOURNAL
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                                                                    Query Match
Best Local Similarity
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Best Local
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                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ746802 483 bp mRNA linear EST 07-JUL-3
AJ746802 forward - stimulated minus unstimulated macrophage Sus
scrofa CDNA clone F_C0001825c_D07, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                         Royal School for Veterinary Studies
Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
Sequencing was performed by ARK genomics. This clone is available
from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9P8,
UK. See www.ark- genomics.org or contact info@arkgenomics.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (Dases 1 to 483)
Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, Jand Dixon, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Hopwood PA
Dept. of Preclinical Veterinary Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development of a porcine cDNA microarray Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (pig)
Sus scrofa
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ACTACATECTTETTCAACCETTCETCTTETTCCATCETCCAAECCTTECCTATTCTEAAC 80
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                                                  Conservative
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                                                                                                                                                                                                              /organism="Sus scrofa"
/mol type="mRNA"
/db xref="taxon:9823"
/clone="F C0001825c D07"
/tisse_type="lung"
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/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
                                                                                                                                                                           /cell_type="macrophage"
/clone_lib="forward - s
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                                                                    Score 32.4;
Pred. No. 20;
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Pred. No. 18;
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AUTHORS
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BE632212/c
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AW990724/c
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BE632212
498 bp mRNA linear EST 25-AUG-2000 uulif01.x1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:3371641 3', mRNA sequence.
BE632212
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uf10b11.x1 Soares mammary_gland_NMLMG Mus
IMAGE:1510941 3', mRNA sequence.
AW990724
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 497)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NRIIONAL CARCET Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other_ESTs: uf10b11.y1
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:937793
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EST.
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                                                                                                                                                                                                                                                                                                                                             TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG
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                                                                                                                                                            GT 369
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: gT773D-Pac (Pharmacia) with a modified
polylinker; let etrand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT732 vector. Library is normalized. Library
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:1510941"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                               20.6%;
54.1%;
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Pred. No. 20;
0; Mismatches
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musculus
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Search completed: September 16, Job time : 496.661 secs
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                                                                                371
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                                                                                                                       147 GT 148
                                                                                                                                                                 431 GTTCTAGATTCCCAAAGAAGCCATTTTGCACTACAGTCAAACATACTAACACCCTGAAAT
                                                                                                                                                                                                          87 GATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCACATAT
                                                                                                                                                                                                                                                                                             27 TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG
                                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Other EST8: uullf01.y2
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 498)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 459.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="soares mammary gland NMLMG"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3371641"
/sex="female (lactating)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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(Otgay) ^{Anolg} eQD9 aiAT

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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
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14440.280 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                   4708233 seqs, 24227607955 residues
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	

		•			SOUTH	
Result No.	Score	Query Match	Length	DB B	ID	Description
1	30	100.0	30	6	AX224397	AX224397 Sequence
N	30	100.0	255	σ	AX224402	AX224402 Sequence
ω	30	100.0	1394	σ	AX224394	
4	30	100.0	1394	σ	AX224395	
Ç,	30	100.0	1394	σ	BD062176	
6	30	100.0	1394	σ	BD062177	Male
7	30	100.0	3343	8	AF360356	AF360356 Zea mays
8	24.2	80.7	158	6	AX224396	AX224396 Sequence
o 9	22	73.3	1304	σ	AX523502	AX523502 Sequence
	21.6	72.0	187192	N	AC124638	AC124638 Mus muscu
11	21.6	72.0	188427	N	AC151282	AC151282 Mus muscu
c 12	21.2	70.7	129778	8	AC091123	AC091123 Oryza sat
13	21.2	70.7	140729	8	AP006548	
14	21.2	70.7	153675	N	AP005710	AP005710 Oryza sat
15	21.2	70.7	155146	8	AP004118	AP004118 Oryza sat
16	21.2	70.7	158374	8	AP004786	AP004786 Oryza sat
	21.2	70.7	172058	8	AP003682	AP003682 Oryza sat
c 18	21.2	70.7	178158	8	AC084320	AC084320 Oryza sat
	21	70.0	91298	N	AC119671	AC119671 Oryza sat

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68.0	68.0	68.0	68.0	68.0	68.0	68.0			68.0	68.0	68.7	68.7	68.7	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	
146776	114051	80413	65406	42868	1985	1913	1882	1762	1542	1026	206372	196303	173088	300029	253492	188854	187707	177790	162198	158839	156394	143681	142015	123472	
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AP007223 Oz	AL606598 Oz	AC021665 Ar	AC115980 Mt	AC067922 Hc	AF242307 Et	AJ252133 Az	X75365 A.thaliana	AY049275 Az	AX506929 Sequence	AJ429890 Human imm	BX005189 Mouse DNA	AC101349 Mus muscu	AC109365 Or	AE017121 Oz	AC102160 Mt	AL626770 Mouse DNA		AP005930 Oz	AP005916 O1	AC090882 O1	AC026558 Hc	AC082645 O1	AC120884 Or	AC120984 Or	
Oryza sat	Oryza sat	Arabidops	Mus muscu	Ното варі	Euphorbia	Arabidops	naliana	Arabidops	equence	Juman imm	fouse DNA	đus muscu	Oryza sat	Oryza sat	Mus muscu	Mouse DNA	Oryza sat	Oryza sat	Oryza sat	Oryza sat	Homo sapi	Oryza sat	Oryza sat	Oryza sat	

ALIGNMENTS

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RESULT 2
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Zea mays
Zea mays
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Sequence 4 from Patent WO0160997.
AX224397
AX224397.1 GI:15554639
                                                          AX224402 255 bp
Sequence 9 from Patent WO0160997
AX224402
                                                                                                                                                                                 1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                            AX224402.1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Albertsen, M.C., Fox, T
Male tissue-preferred
Patent: WO 0160997-A:
                                                       Eukaryota; Viridiplantae; Streptophyta; En
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clade; Panicoideae; Andropogoneae; Zea.
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             Huffman, G. and Kenda and method of using
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BD062176
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Best Local Similarity
Matches 30; Conserv
                               ORGANISM
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PD 30-OCT-2001
PF 19-JUN-1998 JP 1:
PR 23-JUN-1997 US
PI MARC C ALBERTSEN
PI TIMMY L KENDALL
PC C12N15/82,C12N15,
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Sit
CC Topology: Linear;
FH Key
                                                Male tissue-preferred regulatory BD062177 BD062177 BD062177 GI:22607782 JP 2001520523-A/2.
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                           Homo sapiens (human)
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Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Male tissue-preferred regulatory region and Patent: JP 2001520523-A 1 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC
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Male tissue-preferred regulatory
 Mammalia; Eutheria;
               Eukaryota;
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Location/Qualifiers
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23-JUN-1997 US
08/880499
MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMA
TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
                                                                                                                                                                                                                                                      100.0%; Score 30; DB 6 ilarity 100.0%; Pred. No. 0.03; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Strandedness: Single;
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30-OCT-2001
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                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
            Metazoa;
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100.0%; Pred. No. 0.03;
tive 0; Mismatches
Chordata;
Primates;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 7
AF360356
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Matches 30
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                                                                                                                                                                                                      Direct Submission
Submitted (13-MAR-2001) Trait and Technology Development, Pioneer
Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,
IA 50131-1004, USA
                                                                                                                                                                                                                                                                                                                                                                     Zea mays
Zea mays
                                                                                                                                                                                                                                                                                         Fox, T.W., Trimnell, Cloning of Me45, a
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach, Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Clade; Panicoideae; Andropogoneae; Zea.
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Zea mays male fertility protein
AP360356
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Fox, T.W., Trimnell, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                        AF360356.1
                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Albertsen,M.C., Fox,T.W., Garnaat,C.W.,
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x,T.W., Trimnell,M.R.
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TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
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                                                 /product="male fertility protein"
join(1392. .1768,1898. .2182,2280
                                                                                                                        /db_xref="taxon:4577"
/chromosome="9L"
                                                                                                                                                cultivar-"B73"
                                                                                                                                                                       organism="Zea mays"
                                                                                                                                                                                            ocation/Qualifiers
                                     gene="M845"
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                                                                                                                                                          _type="genomic DNA"
                                                                                                                                                                                                                                                                                           gene
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(M845)
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                                                 .2182,2280.
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aceae; PACCAD
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AX523502/c
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AUTHORS
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AX523502
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SRKDHLNILLEGGGTGRLLRYDPETSGVHVVLKGLVFPNGVQISEDHOFLLFSETTNC
RIMRYMLEGGRAGSVEVFANLFGFFDNVRSNGRGOFWVAIDCRTFAADEVFAKRBWLR
TLYFKFPLSLKVLTWKAARRMHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK
LWIGTVAHNHIATIPYPLED"
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Sequence 3
AX224396
                                                                                                                                                                                                                                                                                                                     1 CATGCTTGTTCAACCGTTCGTCTTGTTCC
                                                                                Macina, R.A.,
Compositions
                                           Patent: WO 02064788-A 90 22-AUG-2002;
Diadexus, Inc. (US)
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                     Homo sapiens
                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                             AX523502.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Male tissue-preferred regulatory region Patent: WO 0160997-A 3 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US)
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                         Location/Qualifiers
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Zea mays"
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                                                                              Chen, S.Y., relating to
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          AL Submitted (15-UN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Dases I to 187192)

Biren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Cock, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maudrim, J., Manning, J., Matthews, C., McCarthy, M., Maudrim, J., Manning, J., Matthews, C., McCarthy, M., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Nachen, S., Schupback, R., Seanan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stohanovic, N., Stubbs, M.,
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 17, clone RP23-461H1
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Direct Submission
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Similarity 83.3%;
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/db_xref="taxon:9606"
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Pred. No. 97;
Stojanovic, N., Stubbs, M.
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AC151282 188427 bp DNA 1:
Mus musculus chromosome 17 clone RP23-461H1,
PROGRESS ***, 12 unordered pieces.
AC151282
AC151282.1 GI:51511039
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                            ATGCTTGTACAACAGTTGATCTTGTTCC 52854
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Center clone name: 461_H_1
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/clone_lib="RPCI-23 Female Mouse BAC"
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/chromosome="17"
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6: gap of 100 bp
11: contig of 10055 bp in length
12: gap of 100 bp
9: contig of 23078 bp in length
9: gap of 100 bp
7: contig of 2588 bp in length
7: contig of 2588 bp in length
7: gap of 100 bp
0: contig of 54893 bp in length
0: gap of 100 bp
9: contig of 5679 bp in length
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contig of 33551 bp in length
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contig of 33551 bp in length
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contig of 7235 bp in length
gap of 100 bp
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Wilson,R.K.
Direct Submission
Submitted (24-AUG-2004) (
Parkway, St. Louis, MO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.99019 Consensus quality: 182668 bases at least Q40 Consensus quality: 183763 bases at least Q30 Consensus quality: 184341 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: M_BA0461H01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Mus musculus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                          11125
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4759
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                                                                                                                     organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                             Location/Qualifiers
                                                                           /db_xref="taxon:10090"
                'note="assembly_name:Contig11"
                                                            clone="RP23-461H1"
                                                                                                                                                                 . 188427
                                                                                                                                                                                            11224: gap of unknown length
21177: contig of 9953 bp in length
21277 gap of unknown length
31319: contig of 10042 bp in length
31419: gap of unknown length
54758: contig of 23339 bp in length
54858: gap of unknown length
95804: contig of 40946 bp in length
95904: gap of unknown length
135186: contig of 39282 bp in length
135286: gap of unknown length
135286: gap of unknown length
186833: contig of 51397 bp in length
186783: gap of unknown length
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11224: gap of
21177: contig
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1229: gap of unknown
2832: contig of 1603
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4658: contig of 1726
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 129778)
Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N.,
Gansberger, K., Brenner, M., Burgess, S., Hance, M., Shvartsbeyn, M.,
Tsitrin, T., Riggs, F., Hsiao, J., Zismann, V., Blunt, S., Pai, G.,
Vanaken, S.E., Utterback, T.R., Peldblyum, T.V., Quackenbush, J.,
Salzberg, S.L., White, O. and Fraser, C.M.
Oryza sativa chromosome 3 BAC OSJNBb0093E13 genomic sequence
Submitted (18-JUL-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
                                                            Buell, R.
                                                                           Direct Submission
Submitted (14-JUL-2001) The Institute for Ge
Medical Center Dr. Rockville, MD 20850, USA,
5 (bases 1 to 129778)
                                                                                                                                                                           Submitted (11-JUL-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 129778)
                                                                                                                                                                                                                                                                            Submitted (31-MAR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA 3 (bases 1 to 129778)
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/note="assembly_name:Contig24"
95905. .135186
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31420. .54758
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4759. .6427
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2933. .4658
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186784. .188427
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135287. .186683
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Pred. No. 1.4e+02;
0; Mismatches 4;
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We 3 BAC OSJNBb0093E13 genomic sequence,
                                                                                                Genomic Research,
SA, rbuell@tigr.or
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This BAC overlaps with rice BACs OSUNBa0091J19 (GB:AC084320) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-AUG-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org On Jul 11, 2001 this sequence version replaced gi:14042999. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSJNBb0024J04
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I CEENPODE I FODEEE I DCEEDLDDDDDDCESLDDDNI ECFDAED I I CLETRTMKSST
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/rpt_family="(GAA)n"
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                   /note="predicted by fgenesh"
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Join (4620. 4718,4866. .>5435)

Join (4620. 4718,4866. .5435)
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gene="OSJNBb0093E13.5"
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                                                                                       'gene="OSJNBb0093E13.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="OSJNBb0093E13.4"
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chromosome="3"
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                                                                                                                              _ement(4730. .4835)
family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _family="Gaijin_Os2 MITE element from gb:D10985 Rice
ne_cbp3 gene for carboxypeptidase III (1125 to 1251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _species="japonica"
                                                                                                                                                                                                family="(CGG)n"
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GICEENPDDEISDDVESSNHOHDUDGSNDATEVTTSGEEDLDDESDVEEDTTDLES
GICEENPDDEISDDEEESDPEEED IGSSDLETDSDEY IESTDEESDVEEEDTTDLES
GDSBDTESTSGSHDEDLDDDESLDDDGSSCFDEEDKTGRTENPDDESVOTGSSDEEE
SDDEEDSYSDEEIDDEEESDCDEEIDEEEDEHGGNKYDAIDNESFGEEESVGGSDA
EEMPEFTCVPVSYNDIOTDSDMEIDGGSDEGGNVDAIDNESFGEEESVEDGSDDEEPEFAGGGYDGIDYESLNGDDFEEYLQVLADGGIDNESFGEEESVLDDEVLDFFHGLNDEFL
DFFYGDTLXDYETESSCDEECEHVCVCGGCCKLIDGEESVLDDEVLDFFHGLNDEFL
DFFYGDTLXDYETESSCDEECEHVCVCGGCCKCLITGGEEFYGLTGDEFDGTQLGEEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mote="highly similar to retrofit gag pol protein GB:ANAB2754 GI:2586082 (Oryza longistaminata)" complement (join <12766. .12903,13103. .13518,13741. /gene="OSJNBb0093E13.7" complement (join (12766. .12903,13103. .13518,13741. ./gene="OSJNBb0093E13.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Rice retrotransposon To87 DNA for reverse
transcriptase, partial cds gi|1621482|dbj|D85871.1|D85871"
complement(16049, .16146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKKIYTDGTVKYGCFTSSGEPQNLAEALGDRNWKEAMDKEYYALMKNETWHLVPPKKG
INIIDCKWVYKIKRKADGSLDRYKGRLVAKGFKQRYGIDYEDTSSVVKAATIRTVLS
LVASKOTSLFFYDKNGVTMFMLVYVDDIIVSSSSEKATSALAQDLNQEFALKDLGDH
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DSTQYRSIVGALQYLTLTRPDISFSVNKDPTLYLGVHENKLQFLDQVLKLNTRHWQMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative gag-pol protein"
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GDASGADEEEPSDAGESDHDTAPDAGDGEAHGDSADMAGGNSAAAAAEPASTSSQFQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted by fgenesh" <17933. .>19954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (13497 . .13708)
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/gene="OSJNBb0093E13.7"
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KGRRWSEEGBRKATYSGRALGDGRRRGASSSASGRGRGGRVEGVLRHTPTHAPVPSV
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RAGAVKNAAGAHGRQRRSSSGGKKEKGRVERRGSTMPFWGGREGWERELWLHVLDASA
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/codon_start=1

/product=:hypothetical protein"

/protein_id="AAK72895.1"

/db_xref="GI:14718317"
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17933. .19954
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JOURNAL
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                                                                                                                                                                                                                                    Submitted (08-JUL-2003) Antonio C Oliveira, Universidade Federal de Pelotas, Centro de Genomica e Fitomelhoramento, Department Fitotecnia; Campus Universitario do Capao do Leao, Pelotas, Pelotas, Rio Grande do Sul 96010900, Brasil (8-mail:acostol@terra.com.br, URL:http://www.ufpel.tche.br/faem/fitotecnia/fitomelhoramento/, Tel:55-32-75-9031)

Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), Genemark.hmm (http://www.softberry.com/), Genemark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.biology.gatech.edu/GeneMark/), SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), BLASTN and BLASTN. The genomic sequence was searched against NCBI NonRedundant Protein database no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20209
               (ftp://ncbi.nlm.nih.gov/blast/db) and the EST sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTS represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without such as same name, 'putative-' and '-like protein'. A gene without such as same name, 'putative-' and '-like protein'.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
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Oryza sativa nipponbare genomic DNA, chromosome 9, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                          Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Only in Database (2003)
2 (bases 1 to 140729)
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/rpt_family="AT_rich"
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VGUDVSASNTAAAAFLPDTLALQDGVVSLAVFYLLFGVVYLLLRICALN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="OSJNBb0093E13.8"
/codon_start=1
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21519. .21947
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to any protein but with EST homology (covering
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Pred. No. 2.2e+02;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0705E11 clone has an overlap with OSJNBb0069D16 clone(DDBJ: AP005882)at 5' end and an overlap with OSJNBa0038K02(DDBJ: AP005862) at 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard.
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complement (7148..9310)
/gene="P0705E11.2"
/gene="P0705E11.2"
/note="P0705E11.2"
/no
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VWRTMTRARGLGNPLQSSTIRISVDGRQRLSAPAGYFGNLVLWAFPRATVGDLLGRPL
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/note="probably inactive due to 3' exon missing in CDS
probably inactive due to 5' exon missing in CDS
pseudogene, orf3 of gypsy-type retrotransposon RIRE2"
KHAAQVIHDAVARADAAYFRSFVDFASSGAVEGEGLAPTAVLKDVLCPDLEVDSWLTF
                                                                                                                                                                                                                                                                         DFLVAWGRAARGLAVAATAAAPPHHHPGMFRPRDPPLVEFEHRGVEYYRPPPPAAGVD
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AYFRSFLDFALSGAGGDKEGLAPSAVLKDVLCPNAEVDSWLTFPFYELDFGTGSPTYF
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="9"
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KTGEQGRAMMERNKENAAKKYHHLGSGGYSVAMPKREQMEASLIERGIEPATAMWP
ERSKEWYYAHGGTLNPADGSLVFGYQIGEAARRLTDAVEASSQGTFFRDRDDRDELTLA
LQTPEHFGRTRGKGVIFWKIGFKEDIHTYRSRWASKRDTEAKIADLEFRVSSYELMWQ
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CPVDDITQRTPCELHIPFKNLSIKVASGMAIPTDPSGTYHCRPIPAGSGKSKEVELLVEG
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PSPPHAPPASSPPQAPASTPQDPAPTPRAPTFTPPQAPLPAPSKSRAPPAPFLAHTR
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SASVLKAIKLSDYSTTLKKASSGKKFWPQLGBCPMOREIEPLVTGVAPIEKASVKYWY
ELGKPLVKPELLQSLPTQMYKFHQLYMEMSATGREMIGARIRDTDFLQGDDILWINFR
GIYELYQLDALDVCIMSCWILMEIQRARRRVFDTGFTDPWKVNVAMLDQYPQETEDN
LVHLLKAQHYKTPILLPWTTEETHWVLLIIDLBACTVUNVDSMDKKESTFDKVFGELIDR
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LNRQQSIHPPPAFGSSTNLEDALALEAKSQGQHDSTSDNUYXRPMHETTESTIDKPK
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ETQGWSTTHSWSSFVENMQIGENSAAHHVEIPRASKSWEIDVLLKFGNKVASGSYG
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                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0705E11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="start and end point are not identified"
join(49006. .50427,50502. .51258,51322. .51598,51708. .5
51978. .52088,52173. .52245,52340. .52438,52518. .52703)
/gene="P0705E11.6"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(<57646. .57935,58078. .58192,59352. .59443,59596. .59709,
59896. .59950,60105. .60215,60983. .61036,61119. .61294,
61380. .61487,62089. .62162,62257. .62432,62926. .63021,
63291. .63371,33470. .63523,64003. .64137,64210. .>64290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MADRDKEQILYDTIAEGSSQYWNEEEGNEDPNQYLNEEGNVERD
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SAPAEAAKNYVRHSGWVVRDNVPVSTVYWRRTRARGDHESFVPDSEKEMLWTTMLETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57646. .64290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="reverse transcriptase - like
/protein_id="BAC79156.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFYELDFGGGCPTYFMPSYFPTEGMLFLVPSYLGDGSVDAFVPVFDHNLEAFKQSCYS
IE"
                                                                                                                                                                                                                                                                         /product="putative serine/threonine-protein kinase ctr1"
/protein_id="BAC79157.1"
/db_xref="GI:32490474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0705E11.7"
                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                note="contains EST(s): AU101437(E31530), AU101438(E31530)"
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Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in Database (2002)
2 (bases 1 to 153675)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone: P0646B07
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                                                                                                                                         Similarity
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CATGTTTAACCGTTCGTCTTATTCCA 19405
                                                     CTTGTTCAACCGTTCGTCTTGTTCCA 30
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ilarity 88.5%;
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65979. .84215
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75933. .76241,76395. .76475,76728. .77036,78187. .78573,78721. .795224,79613. .79975,80194. .80424,80691. .81035,81251. .81469,81516. .81572,81735. .82079,82295. .82513,
                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                     /db_xref="taxon:39947"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .153675
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                                                                                                              Score 21.2; DB 2;
Pred. No. 2.2e+02;
0; Mismatches 3;
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A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'uppothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a 'probable 'hypothetical' protein and is included as a misscellaneous feature of the sequence.

The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OJ1148_DOS clone has an overlap with OJ1743_B12_(DDBJ: AP004796) clone at 5' end and with P0017H11 (DDBJ: AP004796) also as 'end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at 'protein and sequency and an entry the sequency of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in Database (2001)
2 (bases 1 to 155146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP004118.4 GI:41053257
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BAC clone:OJ1148_D05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    s available at
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complement (join (15074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="start and end point are not identified" complement(10461. .10670) (gene="0J1148 D05.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <9758. .>9946
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/note="start and end point are not identified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (10461 ..10670)
/gene="0J1148_D05.3"
complement (<10461 ...>10670)
/gene="0J1148_D05.3"
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AIGKLFHSGLAHKAINAMELMEALKEIQTMFVAKHEKEKLIKFATPSTIKPTKW
SYPGGGLNQIPGECTISGDIRLTPFYSTTSVVKKLOBYVHDINENIEKLPTRGFVSKY
VLPDENLRGRLEITIDEDIMNGVACNLESRGFQALCKATEEIVGHVEPYSITGSLPLI
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contains full-length cDNA(s): AK105916,AK101568"
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                                                                                                                                                                                                                                                                                                                                                        gene="OJ1148_D05.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="start and end point are not identified"
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7646. .7703,8300. .8317,8422. .8544,8646. .8802,8884.
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.1"
.15178,17827. .17877,17931. .18029
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Search completed: September 16, 2005, 03:01:24
Job time: 105.667 secs
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Best Local Similarity 88.5%;
Matches 23; Conservative
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/rote"hypothetical ORF
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18062. .18190,18223. .18322,18729. .18861,18967. .19111))
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/codon_start=1
/product="putative basic-helix-loop-helix transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32784. .35862

/gene="OJ1148_D05.9"

/gini(32784. .33234,33666. .34250,35333. .35862)

/gene="OJ1148_D05.9"

/note="supported by full-length cDNA(s): AK060695"

join(32872. .33234,33666. .34250,35333. .35506)

/gene="OJ1148_D05.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein id="BADD7689.1"
/protein id="BADD7689.1"
/db_xref="G1:41053263"
/tzanslation="MPCTSPSCKATICRTPGNHHHGTTSELRAASRRASSLWEEMVLP
/translation="MPCTSPSCKATICRTPGNHHHGTTSELRAASRRASSLWEEMVLP
/translation="MPCTSPSCKATICRTPGNHHHGT"
/translation="MPCTSPSCKATICRTPGNHHHGT"
/translation="MPCTSPSCKATICRTPGNHHHGT"
/translation="MPCTSPSCKATICRTPGNHHHGT"
/translation="MPCTSPSCKATICRTPGNHHGT"
/translation="MPCTSPSCKATICRTPGNHHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30668. .30991
/gene="0J1148_D05.8"
/note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="031148 D05.8"
<30668. .>30991
/gene="031148 D05.8"
/note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this category is not included in IRGSP standard" 30668. .30991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="start and end point are not identified"
complement (join(25292. .25412,25471. .25586))
/gene="0J1148 D05.6"
/note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted by GENSCAN

predicted by GENSCAN

this category is not included in IRGSP standard"

complement (25292. .25586)

/gene="OJ1148_D05.6"

/gene="OJ1148_D05.6"

/gene="OJ1148_D05.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAD07690.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by GENSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon start=1
                                                                                                                                                                                                                                                                                                                                                              Score 21.2; DB 8;
Pred. No. 2.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 155146;
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Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
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                                                                                                                                                                                                              N_Geneseq_16Dec04:*
1: geneseqn1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                             4390206 seqs, 2959870667 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            September 15, 2005, 08:10:17; Search time 14.5242 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catgcttgttcaaccgttcgtcttgttcca 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
geneseqn2003cs:*
geneseqn2003ds:*
geneseqn2004as:*
geneseqn2004bs:*
                                                                      geneseqn2003bs:*
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geneseqn2001bs:*
geneseqn2002as:*
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12227.321 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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20	19	18	17	c 16	c 15	C 14	c 13	12	11	10	9	ი 8	7	6	ហ	4	u	N	۲	Result No.
19.4	19.4	19.4	19.4	19.6	19.6	19.6	19.6	19.6	20	20.2	20.4	22	24.2	30	30	30	30	30	30	Score
64.7	64.7	64.7	64.7	65.3	65.3	65.3	65.3	65.3	66.7	67.3	68.0	73.3	80.7	100.0	100.0	100.0	100.0	100.0	100.0	Query
349980	2243	2243	2240	2000	2000	2000	2000	2000	2000	2397	1542	1304	158	1394	1394	1394	1394	255	30	Query Match Length DB
6	9	4	N	12	8	8	в	œ	12	8	σ	σ	ហ	v	s	N	N	Ŋ	ហ	80
ABQ81845	ACD26214	AAF29956	AAQ47668	ADJ40977	ADA72530	ADA71736	ADA71994	ADA72061	ADJ40785	ACA44013	ABZ13819	ABQ75351	AAH76334	AAH76333	AAH76332	AAX07409	AAX07408	AAH76340	AAH76335	ID
Abq81845 Bifidobac	Acd26214 cDNA enco	Aaf29956 Rat brain	Aaq47668 Sequence	Adj40977 Plant cDN	Ada72530 Rice gene	Ada71736 Rice gene	Ada71994 Rice gene	Ada72061 Rice gene	Adj40785 Plant cDN	Aca44013 Prokaryot	Abz13819 Arabidops	Abq75351 Human lun	Aah76334 Z. mays M	Aah76333 Z. mays M	Aah76332 Z. mays M	Aax07409 Zea mays	Aax07408 Zea mays	Aah76340 Z. mays M	Aah76335 Z. mays M	Description

The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -152 to -181 bases upstream

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A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

Claim 5; Page 47; 50pp; English.

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45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	,
18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	19	19	19	19	19	19	19	19	
62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	
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AAV52265	AAZ61238	ACF79841	ADM02356	ADS57809	ADJ41535	ADJ63835	ACA49918	AAS55583	ABX06821	ACA34769	AAS53644	ADI41918	ADE37244	ADD30938	ABK65288	ACN44010	ADB32792	AAS39832	ABA20915	AAK90190	ADE93879	AAC44356	ADA71777	
Aav52265 Streptoco	Aaz61238 DNA encod	Acf79841 Mouse ani	Adm02356 Human cDN	Ads57809 Bacterial	Adj41535 Plant cDN	Adj63835 Plant lip	Aca49918 Prokaryot	Aas55583 Streptoco	Abx06821 S. pneumo	Aca34769 Prokaryot	Aas53644 Helicobac	Adi41918 Plant tra	Ade37244 Plant yie	Add30938 Plant yie	Abk65288 Arabidops	Acn44010 Human gen	Adb32792 Human nov		Aba20915 Human ner	Aak90190 Human dig	Ade93879 Ixodes sc	Aac44356 Arabidops	Ada71777 Rice gene	

ALIGNMENTS

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RESULT 1
AAH76335
ID AAH7
Z. mays Ms45 male tissue-preferred regulatory region fragment.
                                                                                                                                                                                                                                                                         AAH76335;
                                                                                                                                                                                                                                                                                       AAH76335 standard; DNA; 30
                                                                                                        WPI; 2001-514772/56.
                                                                                                                      Albertsen
                                                                                                                                                               13-FEB-2001; 2001WO-US004527.
                                                                                                                                                                              23-AUG-2001.
                                                                                                                                                                                           WO200160997-A2
                                                                                                                                                                                                         Zea mays.
                                                                                                                                                                                                                       Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.
                                                                                                                                                                                                                                                           29-OCT-2001
                                                                                                                                                  15-FEB-2000; 2000US-00504487.
                                                                                                                                    (PION-) PIONEER HI-BRED INT INC.
                                                                                                                     ă,
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                     FOX TW,
                                                                                                                     Garnaat CW,
                                                                                                                                                                                                                                                                                       ₿₽.
                                                                                                                     Huffman G,
                                                                                                                      Kendall TL;
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RESULT 3
AAX07408
ID AAXC
XX
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AAH76340
ID AAH7
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                                                                                  Query Match
Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                 The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment
                                                                                                                                                                                                                            A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
        AAX07408 standard; DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the TATA box of a Z. nucleotide sequence
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         mays Ms45 promoter fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH76340 standard; DNA;
                                                                                                                                                                                                             Example 5; Fig 8; 50pp; English.
                                                                                                                                                                                                                                                              WPI; 2001-514772/56.
                                                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                                                                               13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                                                 WO200160997-A2
                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                 hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001
                                                  39
                                                                                                                                                                                                                                                                                                                                                                                                        male tissue;
                                                         1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                 seed;
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                   255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                              <u>۸</u>
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 promoter;
                                                                                                                                                                                                                                                                              Fox
                                                                                                                                                                                                                                                                              "WT
                                                                                                                                                                                                                                                                                                                                                                                                        regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 C;
                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mays Ms45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255
                                                                                                                                                                                                                                                                              Garnaat CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                  ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                                                                                           Score 30; DB 5;
Pred. No. 0.0051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 T; 0 U; 0 Other;
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                              Huffman
                                                  83
                                                                                           0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                              Ģ
                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                 Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                              Kendall
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                               1
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RESULT 4
AAX07409
ID AAX0
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
23-JUN-1997;
                                                                                        30-DEC-1998.
                                                                                                                                                                                                                            Ms45; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                                               08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX07409 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ms45; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; maize; hybrid seed; fertility; ss.
                                        19-JUN-1998;
                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                                                                                                                               Zea mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                            AAX07409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and infertile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 22-23; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-105628/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1999
                                                                                                                                   WO9859061-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9859061-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX07408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fox TW,
97US-00880499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00880499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US012895
                                           98WO-US012895
                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue-preferred regulatory region
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0.0063;
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RESULT 5
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Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                   A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                          The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a

 mays Ms45

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                                                                                                                                                         Claim 4; Page
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Best Local
                                                                                                                                          promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 may present sequence represents a nucleic acid sequence encoding an Ms45 may present sequence.
                                                                                                                                                                                                The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a
                                                                                                                                                                                                                                                                                            A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from 2. mays
                                                                                                      Sequence 1394 BP;
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                                                                                                                                                                                                                                                                    4; Page 47; 50pp;
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Matches 26
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                                                                                                              Human; lung; lung specific nucleic acid; LSNA; lung LSP; cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
WO200264788-A2
                                           Homo sapiens
                                                                                        LSP; cytostatic; gene therapy; vac squamous cell carcinoma; gene; ss.
                                                                                                                                                                                 Human lung specific nucleic acid sequence SEQ ID NO:90
                                                                                                                                                                                                                                 05-NOV-2002
                                                                                                                                                                                                                                                                                                                         ABQ75351 standard;
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    mays M845 male tissue-preferred regulatory region fragment.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGCTTGTTCAACCGTTCGTCTTTGTTC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 BP; 41 A; 50 C; 21 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>გ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                         cDNA; 1304
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Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                         vaccine;
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                                                                                                         specific protein;
lung cancer;
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RESULT 9
ABZ13819
ID ABZ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The present invention describes an isolated lung specific nucleic acid CC (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid CC sequences comprising 17 - 733 amino acids, given in ABB52873 to ABB52895; CC (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), CG given in AB075262 to ABQ75376; (c) selectively hybridises to (a) or (b), CC or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific CC protein (LSP) sequences have cytostatic activity and can be used in gene CC therapy and vaccines. LSNAs and LSPs are useful for diagnosing and CC monitoring the presence and metastases of lung cancer in a patient. An antibody that specifically binds to an LSP can be used for determining CC the presence of an LSP in a sample, as well as for treating a patient CC with lung cancer, particularly by inducing an immune response against the CL lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs CC imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                        24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New lung
treating
                                                                                24-AUG-2001;
                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                             Arabidopsis thaliana;
                                                                                                                                                                                                                       Arabidopsis thaliana stress regulated gene
                                                                                                                                                                                                                                                    21-JAN-2003
                                                                                                                                                                                                                                                                                ABZ13819;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1304 BP; 352 A; 347 C; 314 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                           28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancerous disease states
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(SCRI ) SCRIPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific nucleic acid useful in gene therapy or as vaccines lung cancer (e.g. squamous cell carcinoma) or non-cancerous, as well as for diagnosing, monitoring or staging these
                                                                                                                                                                                                                                                                                                                                                                                             CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                         standard; DNA; 1542
                                                                                                                                                                                                                                                                                                                                                                               CTTTCTTGTTCCCCCGTTCCTCTTGTTCCA 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                        2000US-0227866P.
2001US-0264647P.
2001US-0300111P.
                                                                                2001WO-US026685
                                                                                                                                                                                                                                                   (first entry)
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RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%;
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                                                                                                                                                                                             plant; gene; stress; transgenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 T;
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                                                                                                                                                                                                                         SEQ ID NO 1624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1304;
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RESULT 10
ACA44013
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to about the present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas putida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates cell has been exposed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; ds; prokaryotic essential gene; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prokaryotic essential gene #25670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA44013 standard; DNA; 2397 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      design;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
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                                                                                                                                                                                                                                            ELITRA PHARM
                                                                                                    ABU40143.
                                                                                                                                                                    Zamudio C,
Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Carr G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81;
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Forsyth
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                                                                                                                                                                       Zyskind JW,
Xu HH;
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Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; cannola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance;

plant nutrition; apical dominance; dwarfism;

early flowering; antiviral;

26-SEP-2001; 2001US-0325277P 26-SEP-2001; 2001US-0325448P

26-SEP-2002;

2002US-00260238

Eukaryota. antifungal

US2004016025-A1

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ADJ4071 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ40785 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant cDNA #1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ40785;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 CATGCTGGTACAACCGTTCGGCTTG
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88.0%;
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Pred.
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1e+02;
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RESULT 12
ADA72061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            or constitutive transcription of an operatively linked nucleic acid
segment. The invention also relates to a method for augmenting a plant
genome and a method of identifying a gene, where its expression is
altered in the seed, leaf, stem, paniale, pollen, root or is constitutive
in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
sorghum, rice or wheat. The polynucleotides and the polypeptides they
encode are useful for manipulating crop plants to alter or improve
phenotypic characteristics, to produce large quantities of oil or
proteins, to incur resistance to insecticides, viruses or fungi, and to
incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
have a high nutritional value with reduced apical dominance or dwarfism,
early flowering or altered metabolic pathways. This sequence represents a
plant nucleic acid of the invention. Note: The sequence data for this
patent did not form part of the printed specification but was obtained in
electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 23
               WO2003000898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantitles of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                              Oryza sativa
                                                                                                                           Rice gene, SEQ ID 5386.
                                                                                                                                                                                            ADA72061;
                                                                                                                                                                                                                         ADA72061 standard; DNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2000 BP; 552 A; 438 C; 444 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or constitutive transcription of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to plant nucleotide sequences that direct seed., leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Budworth P, Moughamer T, Briggs SP, Cooper B, Goff SA, Katagiri F, Kreps J, Provart N, Ricke
                                                                                             Plant; bacterial infection;
                                                                                                                                                             20-NOV-2003
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(GOFF/)
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(MOUG/)
(BRIG/)
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GOFF S A.
KATAGIRI F.
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BRIGGS S P.
COOPER B.
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PROVART N.
RICKE D.
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                                                                                                                                                                                                                                                                                                      TACATGITTAACCGITCGICTTATICAA 1206
                                                                                                                                                                                                                                                                                                                                     TGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
82.1%;
                                                                                           fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   566 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
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e D, Zhu T;
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ADA71994/c
ID ADA719
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Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang H,
Katagiri
                    WPI; 2003-175290/17.
                                                                                                                                                   03-JAN-2003
                                                                                                                                                                                                Oryza sativa
                                                                                                                                                                                                                      Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.
                                                                                                                                                                                                                                                        Rice gene, SEQ ID 5319
                                                                                                                                                                                                                                                                                                       ADA71994;
                                                                                                                                                                                                                                                                                                                             ADA71994 standard; DNA; 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying at least pathogenic infection bacterial, fungal or
                                                                                                     22-JUN-2001; 2001WO-IB001105
                                                                                                                            22-JUN-2001; 2001WO-IB001105
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                                                                              (SYGN ) SYNGENTA PARTICIPATIONS
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F, Quan S,
                                         Chen W,
F, Quan
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO 5386; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
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                                         Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                             65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No. 1.8e
0; Mismatches
                                          Glazebrook J, G
Whitham S, Xie
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le Z,
                                                      Goff SA,
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Zhu
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Identifying at least one gene involved in plant resistance or response to

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RESULT 14
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Best Local :
                                                                                                                                                                                                                                                                          Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                 Identifying at least pathogenic infection bacterial, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                        The present
                                                                                                                                       Claim 27; SEQ ID NO 5061;
                                                                                                                                                                 gene expression.
                                                                                                                                                                                                                                              WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; bacterial infection; fungal infection; viral infection; rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice gene, SEQ ID 5061.
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22; Conserv
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S, Tao
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                                                                                                                                                                            one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
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                                                                                                           relates to
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Pred. No. 1.8e+02;
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Whitham S, Xie
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                                                                                                     a method (M1) for identifying
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e Z, Zhu
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on. M1
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RESULT 15
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Katagiri
                                                                                         The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                             Identifying at least pathogenic infection bacterial, fungal or
                                                                                                                                                                                                 Claim
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Sequence 1; Appli
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5455, Ap	11034 A	820 App	178197,	169, App	17504, A	15779, A	13614, A	17490, A	12574, A	13439, A	9, Appli	16645, A	12327, A	 Appli 	193, App	174, App	204030,

ALIGNMENTS

SEQUENCE CHARACTERISTICS: LENGTH: 1394 base pairs LENGTH: 1394 base pairs CHARACTERISTICS: STRANDEDNESS: single TOPOLOGY: linear HOLECULE TYPE: DNA (genomic US-08-880-499-1 US-08-880-499-1 Sequence 1, Application US/08880499 Patent No. 6037523 GENERAL INFORMATION: APPLICANT: Albertson, Marc C. APPLICANT: Fox, Tim W. APPLICANT: Carl, Garnaat W. CITY: Johnston STATE: Iowa COUNTRY: USA ZIP: S0131 ZIP: S0131 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/880,499 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REGISTRATION NUMBER: 0578 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800 TELEPAX: (515) 248-4844 INFORMATION FOR SEQ ID NO: 1: APPLICANT: Huffman, Gary A. APPLICANT: Kendall, Timmy L. TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION TITLE OF INVENTION: AND METHOD OF USING SAME NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. STREET: Box 1000 DNA (genomic)

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100.0%; Score 30; DB 3; 1 ilarity 100.0%; Pred. No. 0.0009; Conservative 0; Mismatches 0;

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                                                                                                                                                            Patent No. 5319073
GENERAL INFORMATION:
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APPLICANT: Albert
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TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/08/880,499
CURRENT APPLICATION NUMBER: US/08/880,499
                                               APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
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APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUB-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
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CORRESPONDENCE ADDRESS:
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STREET:
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STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
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                                    ADDRESSEE:
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               E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 30; DB 3; llarity 100.0%; Pred. No. 0.0009; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albertson, Marc C.
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RESULT 4
US-08-029-170-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 23;
                                                                                                                                                                                                         Patent No. 6169173

GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08029170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION NUMBER: US 07/861,769
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/928
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                        CLL
STATE: USA
COUNTRY: USA
TTP: 22313-0299
TRADABLE F
            ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: rat brain CCKB receptor FEATURE:
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: \COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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PatentIn Release #1.0,
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                                                                                                                                                        Suite 500
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 Version
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#1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992

CURRENT APPLICATION DATA:
NUMBER: US/08/029,170

APPLICATION NUMBER: FILING DATE: 199303

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US-09-443-745-15
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                                                                                                                                                                                                                                                                                                                           Sequence 15, App. - 800 No. 6706493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/831

FILING DATE: 07-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 4039:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
                                                                                                                                                                                        NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/861,769 FILING DATE: 01-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
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                                                                                                                                                                          Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCTTGCTCAACTCTACGTCTTGTTTC
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                                                                                                                                                                                                                                                                                                                                                    Application US/09443745
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Pred. No. 49;
                                                                                                                                                                                            Suite 500
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US-09-949-016-16262
                                                                            ; ORGANISM: Human
US-09-949-016-16262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-443-745-15
                                                                                                                                                                                           CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                            SOPTWARE: FastSEQ
SEQ ID NO 16262
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16262, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831
PILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)63-4109
                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                            TYPE: DNA
                                                                                                                                LENGTH: 45571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE: 11-AUG-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
          Conservative
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136..1494
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79.3%;
                          63.3%;
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       Score 19; DB 4; Le
Pred. No. 1.3e+02;
Pred. No. 1.3e+02;
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Pred. No. 4
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                                          Length 45571;
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            Indels
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          <u>,</u>
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          Gaps
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1438
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US-09-368-590-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-1438/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-368-590-1
 Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                            SOFTWARE: FASTSEQ
SEQ ID NO 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1438, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09368590 Patent No. 6187563
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Solimena, Michele
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
FILE REFERENCE: 101918-200 (CCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER: OF SEQ ID NOS: 8
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                               PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (2266)...(2268)
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LOCATION: (1021)...(1023)
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LOCATION: (100)...(102)
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LOCATION: (1)...(6879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                             LENGTH: 8756
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   Conservative
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                                                                                                                                                                                                    2000-09-08
                                                                                                                                                                                     207012
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76.7%;
                  62.7%;
 Score 18.8; Di
Pred. No. 1.2e
0; Mismatches
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1.2e+02;
7;
                                   DB 4;
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OF DETECTION AND USES THEREOF
                                   Length 8756;
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US-09-949-016-13180/c
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                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PRILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76./
23; Conservative
                                                                                                                                                                                                                                                               Sequence 13180, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PH
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Charles TITLE OF INVENTION:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double
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36,373
PB340P1
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US-09-270-767-13492/c
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; ORGANISM: Drosophila melanogaster
US-09-270-767-29480
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US-09-270-767-29480/c
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION SOUTHARE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOUTWARE: Patentin Ver. 2.0
SEQ ID NO 29480
LENGTH: 549
                                                                                                                                                          APPLICANT: Homburger et al.

TITLE OF INVENTION: Nuclaic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13492

LENGTH: 1120
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence 13492, Application US/09270767 Patent No. 6703491
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Best Local Similarity
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SOFTWARE: FREUSEQ for Windows Version
SEQ ID NO 13180
LENGTH: 112874
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                                                                                                                        ORGANISM: Drosophila melanogaster 09-270-767-13492
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LOCATION: (1)...(112874)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Human
                                                                                                                                                       TYPE: DNA
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TECTTETTEAAGAGTTCTTCTTGTT 199
                              TECTTETTCAACCETTCGTCTTGTT 27
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                                                             Conservative
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76.7%;
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                                                             0; Mismatches
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Pred. No. 8
                                                                          Score 18.6;
Pred. No. 9
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Pred. No. 1.
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US-09-573-080A-7/c
; Sequence 7, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GEN
; FILE REFERENCE: 30307
                                                                                                                                                                                          FEATURE:
NAME/KEY: repeat region
LOCATION: (1)..(2710)
COTHER INFORMATION: charlie3
NAME/KEY: misc_feature
OTHER INFORMATION: n is a, c, g or t
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution
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                                                            US-09-573-080A-7
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Best Local S
Matches 22
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SEQ ID NO 3293
LENGTH: 1260
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3293, Application US/09248796A Patent No. 6747137
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                               ISSUE: 4
PAGES: 286-291
DATE: 1992-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                         DATABASE ACCESSION NUMBER: Database
DATABASE ENTRY DATE:
DATABASE ENTRY DATE: 1996-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Candida albicans
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78.6%;
  60.7%;
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Score 18.2; DB 4;
Pred. No. 1.7e+02;
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Pred. No. 1.2e+02;
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                  Length 2710;
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Gaps

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Oy 3 TCCTTGTTCAACCAGTTCGTCTTGTT 27

Db 1209 TGCTGTTCACCAGTTCGTCTKGTT 1185

RESULT 15
US-09-449-016-200252/c
Sequence 200252/c
Sequence 200252/c
Sequence 200252/c
Sequence 200252, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION: PDCIMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PDCIMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PDCIMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PDCIMORPHISMS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CUREENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DA
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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10230.248 Million cell updates/sec
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1 /cgn2 6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*
2 /cgn2 6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*
3 /cgn2 6/ptcdata/2/pubpna/US06_NEW_PUB.seq:*
4 /cgn2 6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*
5 /cgn2 6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*
6 /cgn2 6/ptcdata/2/pubpna/PCT07_NEW_PUB.seq:*
7 /cgn2 6/ptcdata/2/pubpna/PCT08_PUBCOMB.seq:*
7 /cgn2 6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
8 /cgn2 6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                         / Cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USOA_PUBCOMB.seq:*
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o o	Result No.
4864B96	
24 30 24 22 21	1
100.0 100.0 100.0 100.0 100.7 73.3 70.0	Query
30 255 1394 1394 1394 158 1504 1980090	Query Match Length DB ID
2200220	80
100.0 30 20 US-10-713-381-4 100.0 255 20 US-10-713-381-9 100.0 1394 20 US-10-713-381-1 100.0 1394 20 US-10-713-381-2 80.7 158 20 US-10-713-381-3 73.3 1304 13 US-10-001-857-90 70.0 1980090 20 US-10-719-993-6815	ID
Sequence 4, Appli Sequence 9, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 90, Appl Sequence 6815, Ap	Description

5230	5	174	61.3		45	
3242,	9 US-09-974-300-324	375	62.0		44	ဂ
e 497	21 US-10-472-928-4	2162598	62.7	æ	43	ი
e 132,	17 US-10-158-844-13	9541	62.7	18.8	42	
132,	8 US-08-961-5	9541	62.7	8	41	
64, AI	US-10-756-149-6	8788	62.7		40	ი
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33483,	US-10-369-	2247	62.7	8	38	ი
Sequence 2535, Ap	17 US-10-260-238-2535	2000	62.7	8	37	a
e 37788,		1902	62.7		36	ი
9220, A	9 US-09-815-242-9220	1902	62.7	8	35	ი
2217,	US-10-	1899	62.7	18.8	34	ი
e 40048,	US-10-	1856	62.7	٠	33	
	8 US-10-	1125	62.7	8	32	ი
2194,	US-10-335-977-2	1083	62.7	8	31	ი
e 22639	17 US-10-282-122A-22639	1083	62.7	8	30	ი
7281,	9 US-09-815-242-7281	1083	62.7	•	29	ი
971,	2 US-10-	883	62.7	٠	28	a
e 183,	US-10-225-068-183	883	62.7	٠	27	O
381,	7 US-10-374-780A-38	883	62.7	٠	26	ი
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183,	7 US-10-	883	'n	18.8	24	ი
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7	US-09-764-872-7	5671	ω	19	21	Ω
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6	19 US-10	2256646	4.	19.4	17	
e 15, Ap	US-09-443-	2243	4.	19.4	16	
e 1977,	US-10-260	2000	5	19.6	15	ი
e 3534,	-10-425-115-3	901	5	9	14	ი
ID.	US-10-437-963-966	640	5	19.6	13	ი
e 1785,	US-10-260-238-1	2000	66.7	20	12	
e 31883,	7 US-10-282-122A-31	2397	7.	20.2	11	
Sequence 1624,	S-09-938-842A-1	1542		20.4	10	
624	US-09-938-842A-162	1542		20.4	9	
acdustruce Tions	VI 00-141-000-1700	100000				(

ALIGNMENTS

RESULT 1 US-10-713-381-4

Sequence 4, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:

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APPLICANT: HABBRISEN, MARC C.
APPLICANT: APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE OF INVENTION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 30
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-4

Query Match
Best Local Similarity 100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQY 1 CATGCTTGTTCAACCGTTGTTCCA 30
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В

CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30

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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
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US-10-713-381-1
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Best Local S
Matches 30
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KUNDALL, TIMMY L.
APPLICANT: KUNDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                              Matches
                                                                                                Query Match
Best Local
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Publication No. US20040221331A1
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 255
TYPE: DNA
ORGANISM: Zea mays
1179 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CATGCTTGTTCAACCGTTCGTCTTGTTCCA
                                                                              30;
                      1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOX, TIMOTHY W.
                                                                            100.0%; Score 30; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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100.0%; Pred. No.
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                                                                            Mismatches
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                                                                                              0.011;
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RESULT 4

US-10-001-857-90/c
Sequence 90, Application US/10001857
Publication No. US20020183500A1
GENERAL INFORMATION:

APPLICANT: Macina, Roberto

RESULT 6

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-2
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US-10-713-381-3
                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 158
TYPE: DNA
ORGANISM: Zea mays
                                                                               Query Match
Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10713381 Publication No. US20040221331A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ALBERTSEN, MARC C.
APPLICANT: GARNART, CARL W.
APPLICANT: HOFMAN, GARY
APPLICANT: HUFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: USING SAME
FILE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEC IN NOC: -26
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Publication No. US20040221331A1
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
CURRENT FILING DATE: 2003-11-14
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PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 24
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25
                                        1 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
                                                                                 Conservative
                                                                                                  80.7%;
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                                                                             Score 24.2; DE Pred. No. 2.2; 0; Mismatches
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Pred. No. 0.011;
0; Mismatches
                                                                                                                          DB 20;
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Sequence 17676, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 17676
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APPLICANT: Liu, Chenghus
APPLICANT: Liu, Chenghus
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
SEQ ID NO 90
**PRIORE: 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6815
LENGTH: 1980090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6815, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISBASE, METHODS OF DETEC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo Bapiens
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ORGANISM: Homo sapien
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Sun, Yongming
Liu, Chenghua
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82.8%;
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83.3%;
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Pred. No. 1.7e+02;
0; Mismatches
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Pred. No. 25;
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GENERAL INFORMATION:
APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
ITILE OF INVENTION: STRESS-REGULATED GENES OF PLA
ITITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
INUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1624
LENGTH: 1542
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
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US-09-938-842A-1624
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                                                                                                                                                                                                                                                                                                                  Sequence 1624, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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LOCATION: (1)...(1980090)
OTHER INFORMATION: n = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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82.8%;
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Pred. No.
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Pred. No. 1.2e+02
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NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1624
LENGTH: 1542
                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 31883
LENGTH: 2397
TYPE: DNA
ORGANISM: Pseudomonas putida
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR PPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-23 PRIOR PILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26 PRIOR F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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ORGANISM: Arabidopsis thaliana
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1 CATGCTTGTTCAACCGTTCGTCTTG 25
                                                                                                    l Similarity
22; Conserv
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Carr, Grant
Carr, Grant
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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Forsyth, R.
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88.0%;
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                                                                                                                                Score 20.2;
Pred. No. 1.6
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Pred. No. 1
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                                                                                                                                   .6e+02;
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                                                                                                                                                                      DB 17;
                                                                                                                                                               Length 2397;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_94716C.1 US-10-437-963-96639
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US-10-260-238-1785
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; LENGTH: 2000
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 60111.NP

CURRENT APPLICATION NUMBER: US/10/260,238

CURRENT FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: US 60/325,448

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/370,620

PRIOR FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 6077
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 96639, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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                                                                                                                               SEQ ID NO 96639
LENGTH: 640
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Query Match
                                                                                                                                                                 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILLING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                       TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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Barbazuk, Brad
Li, Ping
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Cooper, Bret
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82.1%;
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Pred. No. 1.9e+02;
Score 19.6;
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DB 19;
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Length 640;
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RESULT 15

US-10-260-238-1977/c

Sequence 1977, Application US/10260238

Publication No. US20040016025A1

GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrock, Jane
APPLICANT: Glazebrock, Jane
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US-10-425-115-3534/c
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                                                                                                                FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PRILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 3534
LENGTH: 901
                                                           NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1977
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.3%;
Best Local Similarity 84.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3534, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
TYPE: DNA
ORGANISM: Oryza sativa
.10-260-238-1977
                                                                                                                                                                                                                                                                                                              APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 CATGTTTAACCGTTCGTCTTATTCAA 174
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Goff, Stephen A.
Katagiri, Fumiyaki
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Ricke, Darrell
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Pred. No. 2.5e+02;
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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14440.280 Million cell updates/sec
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AC135206 Oryza Bat
AC084290 Homo Bapi
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KEYWORDS	RESULT 2 AX224398 LOCUS DEFINITION ACCESSION		Query Mata Best Loca Matches	N	AUTHORS TITLE JOURNAL FEATURES BOUTCE	SOURCE	NOIS	AX224399 LOCUS DEFINITION		4 4 4 7	42 43	41 41	9 8	37	. U. 4	ω ω • ω κ	31	28 29	27	25	23	20	
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3 4 5	AX224398 Sequence AX224398	AGGATACCTACTCC	imil ; C		Alberts Male ti Patent: PIONEER	Zea mays Zea mays Zea mays Eukaryota; Vi Spermatophyta clade; Panico	2243	AX224399 Sequence		ហហ	տտ	ຫ ຫ	. ம	ஶஶ	יטיט	n UT UT	ហេច	ທທ	ហេប	ហេហ	ரு மு	ທທ	
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	р 97.	CATCTTACTCATGCAAC CATCTTACTCATGCAAC	<u>ი</u>	DNA"	.W., Garnaat,C. regulatory reg 6 23-AUG-2001; NATIONAL, INC. lifiers	eptophyta Liliopsi neae; Zea		ър)997.	ALIGNMENTS				6	1									
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PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
Albertsen, M.C., Fox, T.W., Garnaat, C.W., Male tissue-preferred regulatory region Patent: WO 0160997-A 9 23-AUG-2001;
                                                              Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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a; Poales; Poaceae; PACCAD
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Sequence
AX224394
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Spermatophyta; Magnoliophyta; Liliopsida;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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/organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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Male tissue-preferred regulatory region and Patent: JP 2001520523-A 2 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC PN JP 2001520523-A/2
                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1394)
Albertsen, M.C., Pox, T.W., Garnaat, C.W., Huffman, G.A. and
Albertsen, M.C., Pox, T.W.,
                                                                                                                                         Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
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                                                                                                                                                                          BD062177.1 GI:22607782
JP 2001520523-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP 2001520523-A/1.
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BD062176.1 GI:22607781
                                                               Kendall, T.L.
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ilarity 100.0%;
Conservative 0,
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23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB b; Pred. No. 2.8e-05;
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Pred. No. 2.8e-05;
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ORGANISM
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DEFINITION
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KEYWORDS
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AF360356
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Best Local (
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PF 19-JUN-1998 JP 1
PF 23-JUN-1997 US
PI MARC C ALBERTSEN
PI TIMMY L KENDALL
PC C12N15/82,C12N15
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Si
CC Topology: Linear
FH Key
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Zea mays
AF360356
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fox, T.W., Trimnell, Cloning of M845, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fox, T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
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x,T.W., Trimnell,M.R.
oning of Ms45, a gene
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x,T.W., Trimnell,M.R.
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llarity 100.0%;
Conservative 0;
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19-JUN-1998 JP 1999504910
23-JUN-1997 US 08/880499
MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFMAN,
join(<1392. .1768,1898. .2182,2280. .2447,2534. .>2942)
/gene="M845"
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join(1392. .1768,1898. .2182,2280. .2447,2534. .2942)
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TGELYVADAYYGLMYVGQSGGVASSVAREADGDFIRFANDLDVHRNGSVFFTDTSMRY
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                                                                                                                                                                                                                                  <1392. .>2942
/gene="M845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/chromosome="9L"
                                                                                                                                                                                                                                                                                                          /mol_type="genomic
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         organism="Zea mays"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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fertility protein
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Pred. No. 2.8e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Albertsen, M.C. required for male
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                                                                                                                                                                                                                                                                                                                         DNA"
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(M845)
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AC135206/c
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                                                                                                                    Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA On Jan 11, 2003 this sequence version replaced gi:24635891.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-22874 and at area 19945-33312. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69957-70761, 89836-90416, 98951-99009, 105316-105607, and 133052-133152 are covered by Monsanto only. The nucleotide sequence of this BAC clone was generated by combining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-NOV-2002) Arizona Genomics Institute, University Arizona, 303 Forbes, Tucson, AZ 85721, USA
4 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J., Collura,K. and Thompson,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-OCT-2002) Arizona Genomics Institute, Arizona, 303 Forbes, Tucson, AZ 85721, USA 3 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T. Currie,J., Collura,K. and Thompson,S.
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5 (bases 1 to 13727)
Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T.,
Saski,C., Henry,D., Thompson,S., Simmons,J., Thurmond,S.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC135206 137327 bp DNA linear PLN 16-APR-2003 Oryza sativa (japonica cultivar-group) chromosome 3 clone 071041F02, complete sequence.
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                                                                                                 Syngenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-JAN-2003) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C.,
Collura,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC135206
AC135206.3 GI:27596977
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-APR-2003) Clemson University Genomics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Currie, J., Collura, K. and Thompson, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 137327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWIGTVAHNHIATIPYPLED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLYFKFPLSLKVLTWKAARRMHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK
                      /organism="Oryza sativa (japonica cultivar-group)"
                                                                        Monsanto and Arizona Genomics Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 8; 1
Pred. No. 2.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim, H.-R.,
                                                                                                      Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rambo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rambo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rambo, T.,
                                                                                                    sequencing data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saski, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saski, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Currie, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
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QPILLKCLQDEASSRVRIAALKAVGSFIEYVNDGGDVVKIFRDFVPSILAVVSRQCLAN
QEEDVASIAFEIFDELIESPAPLLGDSVRSIVQFSLEVCSNQELEINIRQQAIQIISW
LVKEKASFLKKHKLVIFILQVMCQFLTETADBEDGSDLAADBSAAEVIDTMAILLPRH
VFPPVLEFASVSFRHINFKYREAAVTSLGVVSEGCCEHLKDKLEDCLKVVLEALKOQE
QMWRGAASFALGQFAEHLQPEILSHYESVLPCILNALEDPSDEVKEKSYYALAAFCED
MGENILFYLDPLMCRLVMSLGSFRNLGETCMSAIGSVAAAAEQAFMYXBEKVLEMMK
GFMVLTNDEDICARARATEVGIVAMAVGRAEMETILPFEIEAAISGFVLDYSELREY
THGFFSNVAEILDSFAQYLLPHVYPLAFSSCULDDGSAVDIDDADSVDNGFSGVSSDD
DVNDEFRVRNISMLTIIADILTAIRAIFPSHAADVLEKQKDILDTVMNIYIKTMREDDD
KEVVAQACTSLADIVADCGFAIIEPYITRLADATLILLRGESCCQVESDGGEDDGDID
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3513. .3727,3812. .3934,4024. .4054,4157. .4216,5088. .5243,
5322. .5411,5484. .5699,5808. .5942,6035. .6538,6622. .6837,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFGIIDILQDYDITKKLEHAYKSFQVNPDYISAVDPKLYSRRFQDFIRRVFIKEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unknown protein"
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13982. .14130,14224. .14354,14459. .14558,15197. .15503)
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GLHRLFADSEPDDAVRDNAAGAIARMIMVQPQSIPLNQILPLVPDVINAFAQVVVSPN
ESDEVKTVVAKAVSHLISVYGQQMQPILSALPPAHANALASFANRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="(japonica cultivar-group)"
complement(638. .9495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16734. .16878
                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
join(21819. .22007,22096. .2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative MITE, Gaijin/Gaigin-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="0J1041F02.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAP06844.1"
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                                                                                                                                                                                                                                                                                                                                                                                               gene="0J1041F02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="putative transposon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="0J1041F02"
                                                                                                                                                                                                                                                                                                                    gene="0J1041F02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="OJ1041F02.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .19454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein"
                                                                                                                                                                                                                                                                                                                                                22206, 23772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTA, En/Spm-like'
                                                                                                                                                                                                                                                                                                                                                .23996, 24523. .24660)
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13826,

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Query Match
Best Local S
Matches 34
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      y Match 76.0%;
Local Similarity 85.0%;
hes 34; Conservative
                                                                                                                          /note="putative MITE, Castaway-like"
complement (59793. .62196)
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DFHDSPDI PLPSNHQRMRNRRGVVLFÅESDDLADAHÅAKDATFTVQEGRLLÞQSSEL
PCLYGHGISNI VÞESVEFQQSSVPHLHREVI SNQLEFSESRÆFBASSFQNQLESNM
PGSI GQI CDTFMSQGI SCVPESSFMVGGTSAS I SSDDLESLVSNGLSÁLKNESTYTA
SVVALLEDTNKVENQMTDKPQKCMEDEVGETCEASVELLADRNHASCSI TGYQLMDECS
RAESVWLLSGKKNNDSCKVEHVQDTWNRLRQCHÞVLÞCDMNHNRSVSGALKRVSRVSD
LI SESDLMLI SCHÞFENDI SDÞSLTÞYTESDGFSYSKQLEMGSI YAQHGLCI FLQDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative MITE, MITE-adh, type D-like" complement (31668. .31815) complement (35049. .49855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown protein"
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VCVVESTWDILRSFAPEEDSHAHAPASRSGGDSACQDAGEEEDDAAAVLTLEELRLGE
TSEETTGTSSLSTTNDDETSSTTTESMFYISNGRFRRKIRSMNRGMLLGSGSFGTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(26563. .26772,27082. .27288,27430. .27537,
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28790. .28874,29560. .30575))
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                                                                                                                                                                                                                                                                                                                                                                                    ATDDGFVDFLQELLFSGTTTTSLGKFVSSGISCGDGSGNISHVKYPTSCISKRRERQARLREVLLPVVPPKLSQSLRGPAFVDYLSSMSQISQLENMQLSECKASSKQRRCRQPRHYLSSGALSLSAEDIGLLAQCSTFSDRRESETIIEQAIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSSCTHASL FESKOHERVOHEL PEVTPKGCOTANLMTĎKYR PETAÄQVCGNSKHVKF
LNEWLKGWDERGHRIKON I VTNGSMNGRSCQOGSDTDY SEDASY ZNVLLI TGPVGCG
KSAAVFACAREQGFNVI ELIMPKTVVE PFLPHIKLLAQTLDLKPDKLHSSHPSI KY
FTRVFVHMIRUS I I SI SAHSSSLSVI KLHCL VNTSDMENGA YVRQKFEEA TKSHGLEK
WSQEEI IGLPI SNISLDPASGTECTABY KOVINKTLL HYTODEDRGFI STILKM
VETTKWPI ILISNKKDP PLPHILAQLVLDETY PSSAELLESHUDMI CKSEGVEI TVPGO
KHILDAFLGRLNKCLSCPSLLDLDAVHSTVPRI MPMDFPCKLSETI YMEI DKTI VTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDEVILVDESPOKKORKGRKNOGAALKVPNRKHCKALESTDGHESCOOLRSSOTOA
VLPQKSPTSVDIDLVTGPSEASPVNDNVDALDNEDKPOLIVDLKSEANIAAEENRRLS
SGKKMHPFFASRKIHKGAGODILNVEDEDMDSLCAFERDPPLCPVHVLYELEVTWPIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27679. .27832
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LEHPFVNRSMRSIRSMRTSSRSNSSILVLLIMMSWPGRTIRYRBAILSTAQSSTPTIA
                                                                                                                                                                                                                                                                                                                                                          39012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WSNKWLIADKSFLGTSTTEQNSAEHADPGKHLANFHDKQNKSKFSSQDVIDVDDECLL
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46447
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                                                                                                                                                                                                                                                    /note="putative MITE, MITE-adh, type G-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="0J1041F02.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                Score 30.4; DB 8;
Pred. No. 0.12;
      Mismatches
                                                                                                                                                                                                                                                                                                                  type M-like"
                                                              Length 137327;
      Indels
   0; Gaps
0;
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                            TITLE
JOURNAL
REFERENCE
AUTHORS
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                                                                                          Direct Submission
Submitted (21-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 55001)
Direct Submission
Submitted (27-MAR-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                        Unpublished
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1 (bases 1 to 55001)
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Homo sapiens 12 BAC RP11-568G5
BAC Library) complete sequence.
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Gennes and Region of sequences similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality strandards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
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STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
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/rpt_family="L2"
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/function="clone overlap"
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                                                                                                                                      110413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-448C18 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 15, 2002 this sequence version replaced gi:24939941.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
     AC148514
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                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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                                                                                                                                      AGGATACATAAGCCAAATCAACCTTTCTTACTAATGCCAC 110374
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                            clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                        clone="RP23-448C18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                 60.0%;
75.0%;
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Pred. No. 43;
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                                                                                                                                                                    Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, B., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Mallikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A., and Green, E.D.
* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 24, 2004 this sequence version replaced gi:45332443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-MAR-2004) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 171940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS PHASE2; HTGS DRAFT.
Papio anubis (olive baboon)
Papio anubis
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: nisc_zoo@nhgri.nih.gov
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sum-of-contigs
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AC148501
AC1485013 GI:50080339
AC1485013 GI:50080339
HTG; HTGS_PHASE2; HTGS_DRAFT.
Callithrix jacchus (white-tufted-ear marmoset)
Callithrix jacchus (callithrix ))))))
                                                                                                                                                                                                                                                                                                                                              Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Guan, X., Gupta, J., Haghighi, P.,
Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C.,
Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q.,
Legaspi, R., Madden, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H.,
Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C.,
Park, M., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N.,
Schueler, M.G., Shah, K., Sison, C., Stantripop, S.,
Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D.,
Young, A., and Green, E.D.
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27; Conserv
                                                                                          Submitted (10-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
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Callithrix jacchus clone
                              Green, E.D
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 10148: contig of 10148 bp in length
10149 10248: gap of unknown length
10249 103123: contig of 92775 bp in length
103024 103123: gap of unknown length
103124 171940: contig of 68817 bp in length.
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                                                                                                                                                                                                                                                                                                                    Comparative Sequencing Initiative
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clone_end:T7
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clone_end:SP6
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ne CH259-368E20,
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COMMENT
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                                                                                                                                                                                      Submitted (09-JUL-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jul 9, 2004 this sequence version replaced gi:46430810.
                                             Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
-_---- project Information
                                                                                                                                Center: NIH Intramural Sequencing Center code: NISC
Center project name: fvw Center clone name: 368E20
                                                                                                                                                               Center
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated out the sequence been trimmed away, and each base is associated with a Phrap-derived quality score.

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the prieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and Sequencing vector; plasmid; n/a; 100% of reads
Sequencing vector; plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 190717 bases at least Q40
Consensus quality: 191709 bases at least Q30
Consensus quality: 192323 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 192735; sum-of-contigs
Quality coverage: 13.33x in Q20 bases; agarose-fp
Quality coverage: 9.96x in Q20 bases; sum-of-contigs

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FEATURES
                                                                         source
                                                                                                                                                                                                                                                                                                            the accession number will be preserved.

1 29309: contig of 29309 bp in length
29310 29409: gap of unknown length
29410 37712: contig of 8303 bp in length
37713 37812: gap of unknown length
37813 40472: contig of 2660 bp in length
40473 40572: gap of unknown length
40573 45724: contig of 5152 bp in length
46573 46574: contig of 1552 bp in length
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47945
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1. .193735
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clone_lib="CH259"
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contig of 29895 bp in length
gap of unknown length
contig of 89982 bp in length
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unknown length
of 2085 bp in length
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                                                                                     Direct Submission

Submitted (07-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Nov 7, 2000 this sequence version replaced gi:7711370.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                       Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 117026)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.5.
                                              www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACU08897 117026 bp DNA linear PRI 07-NOV-Homo sapiens chromosome 5 clone CTD-2235C13, complete sequence. AC008897
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 117026)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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127712. .193735
/note="clone overlaps with GenBank Accession Number
AC148551 clone CH259-256024 (center project name fvv)"
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73759. .103653
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29410._.37712
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103754. .193735
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                                                           72634 AGGARACGGATTARCAAACTATCCACCTTTCTCAAGCAA 72672
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WI-9815 G05428
SHGC-16751 G15410
WI-7171 G06431.
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                                                                                1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                                                                                    57.5%;
Similarity 74.4%;
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/clone="CTD-2235C13"
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12227.321 Million cell updates/sec
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Listing first 45 summaries
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and is derived ecore Pred. No. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

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SUMMARIES	

The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment upstream of the TATA box of

of.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

WPI; 2001-514772/56.

Claim 14; Page 32; 50pp; English.

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) i	20.8	20.8	20.8	20.8	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
	л () і	52.0	52.0	52.0	52.0	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5
1	11000	6620	6620	6620	891	106315	63294	63294	63294	63115	10286	10286	8404	8404	8404	8404	8404	8404	8404	8404	5507	5507	3117	2792	2000
·	по	ע	σ	4	œ	11	12	10	ဖ	10	σ	4	13	13	10	10	10	10	σ	4.	œ	œ	12	12	12
10.10.10.10.10.10.10.10.10.10.10.10.10.1	NTC1272 1	ARN80279	ABK28416	AAS45488	ABZ51893	ACN43966	ADM74534	ADB72677	ADA02939	ADC85419	ABK28147	AAS45308	ADS89516	ADS89242	ADE84152	ADE84076	ADB54088	ADB54216	ABL33595	AAS46500	ABZ10058	ABZ10204	ADM98942	ADM98941	ADJ41594
CONTENTINGUE TON (2 OF	Continuation (2 of		Abk28416 DNA trans	Aas45488 Chemicall	Abz51893 Aspergill	Acn43966 Human gen	Adm74534 Murine ca	Adb72677 Mouse Tle	Ada02939 Mouse Tle	Adc85419 Mouse Tle	Abk28147 DNA trans	Aas45308 Chemicall	Ads89516 Oligonucl	Ads89242 Oligonucl		Ade84076 Human lym	Adb54088 Pretreate	Adb54216 Pretreate	Abl33595 Human imm	Aas46500 Tumour su	Abz10058 Haematopo	Abz10204 Haematopo	Adm98942 Diterpene	Adm98941 Diterpene	Adj41594 Plant cDN

ALIGNMENTS

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RESULT 1
AAH76337
ID AAH7
XX AAH7
XX AAH7
XX AAH7
XX AAH7
XX AAH7
XX Zea
XX Zea
XX Zea
XX WO2(
XX AAH7
XX Hybx
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XX Hybx
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XX HI
XX H
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    mays Ms45 male tissue-preferred regulatory region fragment.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albertsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2000; 2000US-00504487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2001; 2001WO-US004527.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200160997-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnaat CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huffman
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AAH76334
ID AAH7
                        RESULT 3
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                                                                                                          Query Match
Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
AAH76334 standard; DNA; 158
                                                                                                                                                                                         The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -11 bases upstream of the TATA box of a Z. mays MS45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                  A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514772/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2001; 2001WO-US004527
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                                                                                                                                                                                    nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000; 2000US-00504487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hybrid seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M845; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH76336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH76336 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mays Ms45 male tissue-preferred regulatory region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mays Ms45 male-tissue preferred regulatory region nucleotide sequence
                                                           11
                                                                                                                                                                                                                                                                                                                  5; Page 47; 50pp;
                                                                                  _
                                                                                                           40;
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                                                                                                                     Similarity
                                                                                                                                                          50
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                                                                                  AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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M
                                                                                                                                                                                                                                                                                                                                          fertility in a
                                                                                                                                                                                 ведчепсе
                                                                                                                                                         BP; 18 A; 17 C; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Silarity 100.0%; For Conservative 0;
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dB.
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                                                                                                                                                                                                                                                                                                                                                                                                                Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 14 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                Garnaat CW,
                                                                                                                                                                                                                                                                                                                                          male plant.
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 ВP
                                                                                                          0,
                                                                                                                     Score 40;
Pred. No.
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Pred. No. 3.6e-06;
                                                                                                                                                         G; 10
                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                         T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                Huffman
                                                                                                                                  DB 5;
                                                                                                                                                         U; 0 Other;
                                                                                                                     .7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                <u>ڻ</u>
                                                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                 Kendall
                                                           50
                                                                                  40
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                                                                                                          Indels
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                                                                                                         Gaps
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RESULT 4
AAH76340
ID AAH7
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Best Local Similarity
Matches 40; Conserv
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                                                                                        Me45;
                                                                                                               mays Ms45 promoter fragment.
                                                                                                                                      29-OCT-2001
                                                                                                                                                             AAH76340;
                                                                                                                                                                                   AAH76340
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z. mays Ms45
                                WO200160997-A2
                                                      Zеа таув.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ms45; male tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001
                                                                            hybrid
                                                                                                                                                                                                                                                                                                                                                            nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAH76334;
                                                                                        male tissue;
                                                                                                                                                                                                                                            98
                                                                             seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seed;
                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                            AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 125
                                                                                                                                                                                                                                                          AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                       100.0%;
ilarity 100.0%;
Conservative (
                                                                             promoter;
                                                                                                                                                                                                                                                                                                                                     BP; 41 A; 50 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-00504487.
                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W.
                                                                                        regulatory region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory region; transcription; male fertility;
                                                                                                                                                                                   DNA;
                                                                                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garnaat CW,
                                                                                                                                                                                    ВÞ
                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                       Score 40; DB
Pred. No. 4.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                     21 G; 46 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huffman
                                                                                        transcription;
                                                                                                                                                                                                                                                                                                   4.4e-06;
                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                     0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                              Length 158;
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                                                                                        male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment.
                                                                                        fertility;
                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                   upstream of
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                              The
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23-AUG-2001.

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is
                                                                           New nucleic - useful in
                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX07408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                 WPI; 1999-105628/09.
                                                                                                                                                                                            23-JUN-1997;
                                                                                                                                                                                                                     19-JUN-1998;
                                                                                                                                                                                                                                             30-DEC-1998
                                                                                                                                                                                                                                                                    WO9859061-A1
                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                          Zea maye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 8; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514772/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2001; 2001WO-US004527
                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-)
                                                                                                                                                                                                                                                                                                                     male; tissue-preferred;
tissue; differentiated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                            Me45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
                                                                                                                                         Š,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š,
                                                                       acid encoding a M845 male tissue-preferred regulatory region mediating plant fertility, especially hybrid seed production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                   22-23;
                                                                                                                                                                                                                                                                                                                                                            male
                                                                                                                                                                                          97US-00880499
                                                                                                                                         FOX TW,
                                                                                                                                                                                                                     98WO-US012895
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                                                                                                                                                                                                                                                                                                                                                         tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 1394
                                                  39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                         Garnaat
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                                                                                                                                                                                                                                                                                                                     regulatory region; plant cells; maize; hybrid seed; fertility; ss
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Pred. No. 4.7e-06
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                                                                                                                                         Huffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                         GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kendall
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                                                                                                                                         Kendall
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RESULT 6
AAX07409
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                                    Query Match
Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue-preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin, Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                                                                                                                                                                                                          New nucleic acid encoding a - useful in mediating plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ms45; male; tissue-preferred; plant tissue; differentiated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX07409 standard;
                                                                                           Sequence 1394 BP;
                                                                                                                                                                                                                                                                 Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                                                                                                                                                      WPI; 1999-105628/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX07409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and infertile plants
                                                                                                                                                                                                                                                                                                                                                                  Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9859061-A1
                                                                                                                                                                                                                                                                                                                                                                                             (PION-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1239
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                                    40;
                                   Similarity 100.
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              PIONEER HI-BRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                      plants
                                                                                                                                                                                                                                                                                                                                                                  FOX TW,
                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00880499
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US012895
                                                                                           411 A; 309 C; 232 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                100.0%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                              INI
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                                                                                                                                                                                                                                                                                                                                                                  Garnaat CW,
                                    0
                                                                                                                                                                                                                                                                                           M845 male tissue-preferred regulatory region fertility, especially hybrid seed production.
                                                                                                                                                                                                                                                                                                                                                                                              INC
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory region; plant cells; hybrid seed; fertility; ss.
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Huffman
                                                                                             442 T; 0 U; 0 Other;
                                    6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.1e-06;
                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                  GA,
                                                               Length 1394;
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                                      Indels
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1239

AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278

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RESULT 8
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                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                comprising nucleotide sequences essential for initiating transcription the M945 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
           WO200160997-A2
                                                                                            Z. mays Ms45 male tissue-preferred regulatory region
                                                                                                                     29-OCT-2001
                                                                                                                                                                                                                                                                                                                            Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;

    mays Ms45 male tissue-preferred regulatory region encoding

                                 Zea mays.
                                                                    M945; male tissue;
                                                                                                                                            дан76333;
                                                                                                                                                                    AAH76333 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 46; 50pp; English.
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                                                          hybrid seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a male tissue-preferred regulatory region (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001; 2001WO-US004527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybrid seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ms45; male tissue;
                                                                                                                                                                                                                                 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-514772/56
                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                               AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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                                                                                                                                                                                                                                                                               Conservative
                                                           ds.
                                                                                                                     (first
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                                                                                                                                                                    DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory region; transcription; male fertility;
                                                                    regulatory
                                                                                                                     entry)
                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garnaat CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INT INC
                                                                                                                                                                                                                                                                               <u>.</u>
                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
                                                                    region; transcription;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huffman
                                                                                                                                                                                                                                                                                          6.1e-06;
                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising nucleotide the MS45 gene useful f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ó
                                                                                                                                                                                                                                                                                                    Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kendall
                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                               Indels
                                                                      male fertility;
                                                                                            encoding
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                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                              DNA.
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                                                                                                                                                                                                                                                                               Gaps
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RESULT 9
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an MS45 male
                                                 Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                        Claim 1;
                                                                                                                     Morris DW;
                                                                                                                                                                        01-MAR-2002;
                                                                                                                                                                                                  28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                                                                                                    WO2003073826-A2
                                                                                                                                                                                                                                                                                                         Cytostatic; carcinoma;
                                                                                                                                                                                                                                                                                                                                Human genomic sequence hCG1639824
                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                      ACN45146;
                                                                                                                                                                                                                                                                                                                                                                                                               ACN45146
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                                                                                         WPI; 2003-328604/31
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2000; 2000US-00504487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2001; 2001WO-US004527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2001.
                                                                                                                                                                                                                             12-SEP-2003
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                                                                                                                                              SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                       SEQ ID NO 1948; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for initiating fertility in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                        2002US-00087192
                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                         lymphoma; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                               226215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 5; 1
Pred. No. 6.1e-06;
); Mismatches 0;
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                                                                and
                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                treatment
                                                                of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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present invention relates to novel DNA and protein sequences which

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RESULT 10
ABZ10202/c
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Best Local :
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The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distringuishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ01861 to ABZ1118 represent specifically claimed nucleotide sequences from the present appointment of the contact of the present of the contact of the contact of the present of the contact of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2001; 2001US-0278333P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K, Braun A, Distler J,
, Piepenbrock C, Adorjan
A, Lipscher E, Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoietic cell proliferation disorder; cytostatic; herapy; lymphocytic leukaemia; acute myelogenous leukaem ne methylation state; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                  NO 342;
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72.5%;
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                                                                                                                                                                                                                                                                                                                                                                         117pp;
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); Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                         English.
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1 P, Grabs
Model F,
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he R, Leu E
V, Otto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia;
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degeneration, arteriosclerosis, ia, Alzheimer's disease, AIDS, e

epilepsy,

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Best Local :
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         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiathritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerrosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphcytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder
                                                                                                                                               Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
                                                                                                                                     methylation
                                                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders allowing for improved and informed treatment of patients
                                                                                                    Claim 1; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic;
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                                                                                                                                                                                                                                                             EPIGENOMICS
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2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system associated gene
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                                                                                                      NO 277;
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85.7%;
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                                                                                                                                                fragment of of diseases
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Pred. No. 1.
                                                                                                    Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3056
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.4e+02;
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                                                                                                      German
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ADB54282/c
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Best Local S
Matches 27
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Matches
                              Query Match
                                                                                                                                       The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent or series of reagents, where the reagent or series of dinucleotides within the target nucleic acid. The molecules of the dinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The NNA (peptide nucleic acid)-oligomers are useful as probes for determining cytostate acids)-oligomers are useful as probes for
                                                         Sequence 7110
                                                                                                 determining cytosine methylation state or single nucleotide polymorphisms. The current sequence is that of the pretreated genomic region of the invention. This sequence is not shown within the
                                                                                                                                                                                                                                                                                                                                                          Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis, diseases. The present
                                                                                     region of the 
specification
                                                                                                                                                                                                                                                                                                                     Claim 32;
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                Local
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27; Conserv
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                  Similarity
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Schmitt A;
   Conservative
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                                                          BP;
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                                                       1818 A; 0
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             54.0%;
85.7%;
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75.0%;
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Score 21.6; D
Pred. No. 1.5e
0; Mismatches
   0
                                                         C; 1721 G;
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Pred. No. 1
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                                                       3571 T; 0 U; 0 Other;
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   Indels
                           Length 7110;
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RESULT 13
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XX ADB86
XX Homo
                                                                                  The invention relates to a method of detecting and differentiating CC between lymphoid cell proliferative disorders associated with at least CC one gene and/or their regulatory regions in a subject by contacting a CC target nucleic acid in a biological sample obtained from the subject with CC at least one reagent or series of reagents that distinguish between CC methylated and non-methylated CC dinucleotides within the target nucleic acid. The genes and/or their regulatory regions are preferably selected CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, CCM71, ELKI, ABLI, APC, BCL2, CCH1, CDKN1A, CDKN1B, CDKN2B, FOS, CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB12, TGFBR2, TP73, CDKN1C, CC GSK1beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the CPG dinucleotides within one or more the sequences, or their complements, CC for determining the cytosine methylation state and or single nucleotide conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma. They are also useful for detecting of a predisposition to, CC differentiation between subclasses, diagnosis, prognosis, treating and/or above mentions a nucleic acid of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; SEQ ID NO 192; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-457621/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2001;
28-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylated CpG dinucleotide; single nucleotide polymorphism; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; lymphoid cell proliferative disorder; methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lymphoid cell proliferative disorder gene derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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2001DE-01064501.
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Query Match Best Local Similarity

54.0%; 85.7%;

Score 21.6; DB 10; Pred. No. 1.5e+02;

Length 7110;

Sequence

7110

BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;

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RESULT 14
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ID ADS895
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                                                                                                                                       The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is used to the exemplification of the invention.
                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting responsiveness of a subject with breast cell disorder, useful for treating or differentiating breast proliferative disorders comprises analyzing methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002; 2002DE-01045779
07-JAN-2003; 2003DE-01000096
17-APR-2003; 2003DE-01017955
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                        genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-348468/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foekens J,
Nimmrich I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; cell proliferative disorder; breast; methylation; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide of the invention SEQ ID NO:596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-2004
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                            ATACCTACTCCCAAACAATCCATCTTAC 31
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Rujan T,
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 596; 104pp;
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                                                          Conservative
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                                                                                                                BP; 1818 A; 0 C; 1721 G; 3571 T; 0
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85.7%;
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Schmitt
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                                                                     Score 21.6;
Pred. No. 1.
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Schmitt M,
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                                                                      .5e+02
                                                                                    DB 13;
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Look MP,
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                                                                                                                                      The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2000; 2000US-0227866P
26-JAN-2001; 2001US-0264647P
22-JUN-2001; 2001US-0300111P
                                                                                                                Sequence 1341 BP;
                                                                                                                                                                                                                                                                                                                                                                 Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
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 288
                  1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA
                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCRIPPS RES INST.
SYNGENTA PARTICIPATIONS
                                                                       Similarity
 AGTCCACCTATTCCCAAACAATCTCTGTGCCTCACACAA
                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1555; 577pp + Sequence Listing;
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                                                         Conservative
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                                                                                                                460 A; 231 C; 319 G; 331 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
       seq length: 0 seq length: 2000000000
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Maximum Match 100%
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Sequence 1, Appli
Sequence 2, Appli
Sequence 5546, Appli
Sequence 65770, Appli
Sequence 184, Appli
Sequence 11868, Appli
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202761,
5447, A
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ALIGNMENTS

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APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAN: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-880-499-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08880499 Patent No. 6037523 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
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100.0%; Score 40;
100.0%; Pred. No.
                            DB 3;
                       Length 1394;
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RESULT 2 US-08-880-499-2

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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
                                                                                                                                                                                       Sequence 5546, Application US/09248796A Patent No. 6747137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
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APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Darwin B
STREET: Box 1000
CITY: Johnston
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STREET: Darwin Building, 7100 N.W. 62nd Ave.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albertson, Marc C.
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PATENT NO. 6812339

PATENT NO. 6812339

GENERAL IMPORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SOCTUBARE: FastSEQ for Windows Version 4.0

LENGTH: 601
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US-09-949-016-65770/c
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 5546
LENGTH: 1071
TYPE: DNA
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65770, Application US/09949016
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version
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85.2%;
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Pred. No. 1.2e+02;
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Pred. No. 51;
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OF DETECTION AND USES THEREOF
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; ORGANISM: Human
US-09-949-016-65770
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                                                                                                                                                                                                                                US-08-945-056-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt FL_genes Version 2.0
SEQ ID NO 184
                                                                                                                                                                                            Sequence 4, Application US/08945056 Patent No. 6077994
                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
                                                                                           GENERAL INFORMATION:
APPLICANT: Coupland, George M.
APPLICANT: Putterill, Joanna J.
TITLE OF INVENTION: Genetic control
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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NAME/KEY: CDS
LOCATION: (231)..(749)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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STATE: Virginia COUNTRY: United States of America COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                      Local Similarity 71.1%;
hes 27; Conservation
                                  STREET: 8th Floc
CITY: Arlington
STATE: Virginia
                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 GGATTCCTGGGCTCAAGCAATCCTCCTGCCTCAGGCAA 377
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Zhou, Ping
Zhou, Ping
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
                                                                                                                                                                                                                                                                                             GGAAATCAACTCCAAAAGAAACCCTCGAAACCATGCAA 663
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Ren, Feiyan
                                                             E: Nixon & Vanderhye PC
8th Floor, 1100 No. 6077994th Glebe Road
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71.1%;
                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                            Score 20.4;
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.4; |
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                               of flowering
                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 973;
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                                                                                                                                                                                                                                                                                                                                                            11; Indels
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; ORGANISM: Human
; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(51770)
; OTHER INFORMATION: n = A
US-09-949-016-13668
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13668
LENGTH: 51770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13668, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 816-4000 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                TYPE: DNA
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POSITION IN GENOME:
MAP POSITION: chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9422083.7 FILING DATE: 02-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02561
FILING DATE: 01.NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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80.0%;
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Pred. No. 85;
0; Mismatches
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Query Match

51.0%;

Score 20.4;

DB 4.

Length 51770;

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US-09-949-016-17420
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US-09-949-016-17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11824, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11824
LENGTH: 126200
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Best Local :
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SEQ ID NO 17420
LENGTH: 84571
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 681233
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                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                            NUMBER OF SEQ
                        NAME/KEY: misc_feature
LOCATION: (1)...(12620
                                                                                        ORGANISM: Human
                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (1)...(84571)
OTHER INFORMATION: n = A,T,C or
                                                                        FEATURE:
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27; Conserv
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                                                                                                                                                                                                         ID NOS:
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71.1%;
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Pred. No. 1.7e+02;
0; Mismatches 11; Indels 0;
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; NAME/KEY: misc feature

; LOCATION: (1).T.(126200)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13193
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US-09-949-016-13193/c
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 27
            CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13193
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Appli
Patent No. 646521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13193, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                APPLICANT:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                 APPLICANT: Ascenzi, Robert TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS FILE REFERENCE: 9128.14
                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Boyes, Douglas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
TYPE: DNA
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Hoffman, Neil
Kloti, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAATCAACTCCAAAAGGAACCTTCAAAATCATGCAA 53096
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Gorlach, Jorn
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71.1%;
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71.1%;
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Pred. No. 1.9e+02;
0; Mismatches 11
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Pred. No. 1.9e+02;
0; Mismatches 11;
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FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(5099)

OTHER INFORMATION: n = A,T,C or
US-10-267-763-5
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; OTHER INFORMATION: "n" indicates any nucleotide (A, US-09-610-040-5
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                                                                                                                                                                                                                                                RESULT 14
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Sequence 88655, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 5099
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APPLICANT: Gorlach,
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: MODULATION OF CHORISMATE SYNTHASE AND CHORISMATE MUTASE
TITLE OF INVENTION: EXPRESSION OR ACTIVITY IN PLANTS
FILE REFERENCE: 2035DIV1
CURRENT APPLICATION NUMBER: US/10/267,763
CURRENT APPLICATION NUMBER: US/10/267,763
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 09/610,040
PRIOR FILING DATE: 2000-07-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Woessner, Jeffrey
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ilarity 88.0%;
Conservative
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Pred. No. 1.1e+02
0; Mismatches
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Pred. No. 1.1e+02;
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 88655
LENGTH: 601
TYPE: DNA
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APPLICANT: Liu, (
APPLICANT: Asund:
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                                                              Matches
                                                                                          Query Match
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TITLE OF INVENTION: No. 6595662el Nucleic Acids and
TITLE OF INVENTION: No. 6595662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                       NAME/KEY: CDS
LOCATION: (160)..(849)
                                                                                                                                                                                                                      LENGTH: 2615
                                                                          Local
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1855 ATACCAGTTCCCANACNAACCATCTCTCCATTGGAA 1890
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                4 ATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                             26;
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                                                                           Similarity
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Asundi, Vinod
                                                             Conservative
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                                                                          50.0%;
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                                                                          Score 20; DB 4;
Pred. No. 1.1e+02;
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Pred. No.
                                                           Mismatches
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                                                             10;
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                                                             Indels
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Search completed: September 15, 2005, 08:25:10 Job time : 9.05048 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 1.0
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10230.248 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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in2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
m2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
m2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9NEW_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USOP_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 700402F	Result No.
244444	Score
100.0	Query
40 50 158 255 1394 1394 85779	Query Match Length DB ID
0000000	BB
20 US-10-713-381-6 20 US-10-713-381-5 20 US-10-713-381-3 20 US-10-713-381-9 20 US-10-713-381-1 20 US-10-713-381-2 20 US-10-713-381-2 20 US-10-719-993-6880	ID
Sequence 6, Appli Sequence 5, Appli Sequence 3, Appli Sequence 9, Appli Sequence 1, Appli Sequence 2, Appli Sequence 6880, Ap	Description

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Sequence 112652, Sequence 126, App Sequence 290, App Sequence 4, Appl1 Sequence 4, Appl1 Sequence 1073, A Sequence 170, App	1948 e 11948 e 11948 e 11948 e 11948 e 11955 e 11956 e 11965 e	equence 31006

ALIGNMENTS

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US-10-713-381-6

(US-10-713-381-6

(US-10-713-38
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AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-5
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/860,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 158
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RESULT 4
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                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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                                                                                             1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                                 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 125
                                                                                                                                                        Conservative
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                                                                                                                                                     100.0%; Score 40; DB 20;
100.0%; Pred. No. 4.2e-06;
ative 0; Mismatches 0;
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RESULT 6 US-10-713-381-2

Sequence 2, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.

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                                                         Query Match
Best Local Similarity
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US-10-713-381-1
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SEQ ID NO 9
LENGTH: 255
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10713381 Publication No. US20040221331A1
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Publication No. US20040221331A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARWART, CARL W.
APPLICANT: HUFFMAN, GARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILLE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION A
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                               LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
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                     1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                                               100.0%; Score 40; DB 20; ilarity 100.0%; Pred. No. 6.4e-06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 20; ilarity 100.0%; Pred. No. 4.6e-06; Conservative 0; Mismatches 0;
                                                                                                                     Length 1394;
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US-10-424-59-31006

US-10-424-59-31006

Sequence 31006, Application US/10424599

Hublication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Car Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B

PILE REFERENCE: 38-21(53223)B
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US-10-713-381-2
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Best Local S
Matches 27
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Publication No. US20040265849A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003.11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6880
LENGTH: 85779
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SEQ ID NO 2
LENGTH: 1394
TYPE: DNA
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CURRENT APPLICATION UNMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(85779)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                            16082 AMACTTACTCCCAMACAATCTATGTCACTCAT 16051
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27; Conserv
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HUFFMAN, GARY
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Conservative 0
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Pred. No. 6.4e-06;
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US-10-424-599-83179
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-10-425-115-143168
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                                                                                            NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 83179
                                                                                                                                                                                                                                                                                           Sequence 83179, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 143168
LENGTH: 294
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SEQ ID NO 31006
LENGTH: 706
                                                                                                           APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 143168, Application US/10425115 Publication No. US20040214272A1
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Best Local S
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APPLICANT: Kovalic David K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: PAT_MRT3847_46127C.1
                                       TYPE: DNA
ORGANISM: Glycine max
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ORGANISM: Glycine
                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: MRT4577_62049C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                             LENGTH: 315
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86.2%;
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Pred. No. 49
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Pred. No. 31;
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; ORGANISM: Homo sapiens
US-10-087-192-1948
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
NUMBER OF SEQ ID NOS: 2059
                                                                                                                                                                                                               PILE REFERENCE:
CURRENT FILING DATE: 2003-09-26
RUMBER OF SEQ ID NOS: 1258
SEQ ID NO 342
LENGTH: 4110
                                                                                                                                                                                                                                                                                                                   Sequence 342, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.5
Matches 29; Conservative
                                                                                  Query Match
Best Local (
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Best Local S
                                                                  Matches
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 226215
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                                                                                  Similarity
                                ATACCTACTCCCAAACAATCCATCTTAC 31
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72.5%;
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81.2%;
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                                                               Score 21.6; DB 20
Pred. No. 1.9e+02
0; Mismatches
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Pred. No. 2e+02;
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Pred. No. 55;
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FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR PILING DATE: 2000-08-24
; PRIOR PILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR PILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR PILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1555
; LENGTH: 1341
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                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana US-09-938-842A-1555
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; Sequence 1555, Application
; Patent No. US20020160378A1
; GENERAL INFORMATION:
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                                                                                                                                  Query Match
                                                                                          Matches
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DC 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
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                                                                                                               Local Similarity
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288
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                                        AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
AGTCCACCTATTCCCAAACAATCTCTGTGCCTCACACAA
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75.0%;
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                                                                                                             Score 21.4;
Pred. No. 1.
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Pred. No. 2
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                                                                                                                                  DB 9;
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RESULT 13

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Sequence 1555, Application US/09938842A

Publication No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF USE
FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1555

LENGTH: 1341

TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1555
Search completed: September 15, 2005, 20:45:52 Job time: 33.0505 secs
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                                                                                                                                                                                            Query Match 53.5%; Score 21.4; DB 11; Length 1341; Best Local Similarity 71.8%; Pred. No. 1.9e+02; Matches 28; Conservative 0; Mismatches 11; Indels 0;
                                                                                           Gaps
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CN317130 AGENCOURT
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A1698201 wa67911.x
AA725064 ai06h07.s
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A1467879 tj78609.x
BF601210 266128 MA
A1382034 ta33905.x
BM027586 GIT000109
CK949745 4074916 B
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CG224225 OG1AG08TV
CC656933 OGWDQ20TM
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1 (bases 1 to 687)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R. W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other GSSS: GGWDQJOTM
Contact: Cathy Whitelaw
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genomic survey sequence.
CC656939
CC656939.1 GI:32060231
                                                                                                                                                                                                                                                                                                                                                                              Email: whitelaw@tigr.org
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Fax: 301-838-0208
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9712 Medical Center Drive,
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/note="Vector: pBCSK:, Site_1: HincII; 0.7-1.5
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                                                                                                                                                                                                                                                  /organism="Zea mays"
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1 (bases 1 to 963)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Wan Aken, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
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Unpublished (2002)
Other_GSSs: OGWDQ20TV
Contact: Cathy Whitelaw
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1 (bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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Fax: 301-838-0208
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Other_GSSs: OGIAG08TH
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.
methylation filtered genomic DNA library"
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/strain="B73"
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4e-05;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Insert Size: 1161
High quality sequence stops: 349
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1161
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ym50g08.rl Soares infant brain IMAGE:51939 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Class: sheared ends
                                                                                                                                                                                                                                                                      Seq primer: M13RP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA
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                                                                                                                                                                                                                           quality sequence stop: 349
Location/Qualifiers
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                                                                              /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="GDB:424875"
/db_xref="taxon:9606"
/clone="IMAGE:51939"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4577"
/clone="IzMMBM80554D15"
/clone_lib="ZMO_7_1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
  /dev stage="73 days post natal"
/lab_host="DH108 (ampicillin resistant)"
/clone lib="Soares infant brain lNIB"
/note="Organ: whole brain; Vector: Lafmio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic D
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Pred. No. 3.4e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Box 8501, St. Louis, MO 63108
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RESULT 6
CO117589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center for Genome Information University of Cincinnati Kettering Lab, 323 Eden Ave., Tel: 1-513-558-6678
Fax: 1-513-558-4505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 bp DNA linear GSS 18-MAY-2003 SM416B1-G07_55_13.abl Spider Monkey genomic BAC library Ateles geoffroyi genomic, genomic survey sequence.
BZ706605
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                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qian,Y., Jin,L. and Su,B.
BAC end sequences of spider monkey
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: subn@ucmail.uc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Qian Y, Jin L, Su B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ateles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ateles geoffroyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BZ706605.1 GI:30843142
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                                                                                                                                                                                                                                                                                                                                                                                                                     BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Spider Monkey genomic BAC library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Genomic DNA was
partially digested with EcoRI, Vector, pBACe3.6,
Recombinants were transformed into DH10B."
                                                                                                                                                                                                                                                                /tissue_type="Skin"
/cell_type="Fibroblast"
/cell_line="AG05352"
                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="black-handed spider monkey"
/db_xref="taxon:9509"
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                                                                                                                                                                                                                                                                                                                                                                      organism="Ateles geoffroyi"
                                                                                                                                                                                                                                                                                                              'eex="Male"
                                                                                                                             59.0%;
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Pred. No. 97;
0; Mismatches
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Pred. No. 1.1e+02;
0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cincinnati,
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                                                       217
                                                                                                                                           Length 375;
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Atelinae;
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Best Local Similarity
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GR Eb01H15.r GR Eb C
mRNA sequence.
CO117589
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 783)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y. Rogers,J. and Bradley,A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium raimondii

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 738)
1 (bases 1 to 738)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                              CR181951 783 bp DNA linear GSS 06-JUL-20 Reverse strand read from insert in 5'HPRT insertion targeting and Chromosome engineering clone MHPN361p21, genomic survey sequence.
                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence; MICER.
                                                                                                                                                                                                                                                                                                                                          CR181951.1 GI:49960800
                                                                                                                                                                                                                                                                                                                                                                CR181951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://genome.arizona.e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 5595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Global assembly of Cotton ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arizona Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="GR_Eb"
//clone="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80.
/organism="Mus musculus"
/mol_type="genomic DNA"
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="floral"
/dev_stage="_3 to +3 DPA"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gossypium raimondii"
/mal_type="mRNA"
/db xref="taxon:29730"
/clone="GR_Eb01H15"
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77.8%;
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Pred. No. 1.8e+02;
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GR__Eb01H15 3',
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RESULT 9
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AUTHORS
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                                                                CD495749 1253 bp mRN
CDA18-D05.yld-s SHGC-CDA Gasterosteus
CDA18-D05 3', mRNA sequence.
CD495749
CD495749 1 GI:31422780
EST.
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                   Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1018)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
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CL109241.1 GI:40602876
CSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 72 High quality sequence stop: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: Sp6 ATTTAGGTGACACTATAG Class: BAC ends
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus tropicalis
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28; Conservative
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                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DN
/db_xref="taxon:8364"
/clone="ISB1-51D14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="MHPN361p21"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Xenopus tropicalis"
|mol_type="genomic DNA"
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77.8%;
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; Pred. No. 1.9e-
0; Mismatches
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Pred. No. 1.8e+02;
0; Mismatches 8;
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tropicalis genomic clone ISB1-51D14,
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L.9e+02;
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                                                                                                                                     aculeatus
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AZ883408/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                         1047
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-189L2.TV
Contact: Shaying Zhao
                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 405)
                                                                                                                                                                                                                                                                         RPCI-23-189L2.TJ RPCI-23
                                                                Zhao, S., Nierman, W., Feldblyum, T., Akinret, B., Levins, M., Mcgann, S., Jong, P. and Fraser, C.M.
                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                     genomic survey sequence
                                                                                                                                                                                      Mus musculus (house mouse)
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GI:13202353

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Tsegaye,G.,

Shatsman,S., Geer,K., F

Krol,M.,

405 Mus

musculus genomic

linear (

05-MAR-2001

0

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Indels

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Gaps

<u>,</u>

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HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford,
Tel: 650 725 5954
Fax: 650 725 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsley,D.M., Peichel,C., Balabahdra,S., Schmutz,J. and Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kingsley, DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
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                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence start: 15 quality sequence stop: 667. Location/Qualifiers
                                                                                                                                                                                                  /clone libe"SHGC-CDA"
/clone libe"SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRl
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRl
/note="Vector: lambda ZAP Express/pBK-CMV; The mixed
cyan cDNA library was generated using the ZAP-CDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an oligo dT sequence
preceeded by a synthetic Xhol site. 5 prime adaptors were
used containing an EcoRl cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lacZ promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kingsley@cmgm.stanford.edu
                                                                                                                                             used to generate individual pBK-CMV phagemid clones for EST sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="heads and
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Salinas river,
/db_xref="taxon:69293"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Gasterosteus aculeatus"
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                           58.0%;
77.8%;
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Score 23.2; DB (
Pred. No. 2e+02;
0; Mismatches
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                                                          Length 1253;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 189 row: L column: 2
Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 798)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG506830.1 GI:13468347
EST.
                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601861443F1 NIH_MGC_77 Homo sapiens
                                                                                           CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM916 row: e column: 11
High quality sequence stop: 2.
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG506830
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301 838 0208
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/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-189L2"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C578L/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
/organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 1.9e+02;
0; Mismatches 10; Indels
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Rockville, MD 20850, USA
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BF143726
LOCUS
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Best Local Similarity 74. Matches 29; Conservative
                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 968)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 3
High quality sequence stop: 648.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. CONBORTIUM (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
http://imagg.llnl.gov
Plate: LLAM9274 row: k column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      968 bp mRNA linear EST 24-OCT-2000 6017995601671 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020600 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BF143726
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/clone="IMAGE:4071154"
/lab host="DH108 (T1 phage-resistant)"
/clone lib="NIH MGC 77"
/sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc); S' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACGTCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb) . 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                            /lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/clone_lib="NCI_CGAP_Lu30"
/note="Forgan: lung; Vector: pcMV-SPORT6; Site 1: Noti;
/note="Forgan: lung; Vector: pcMV-SPORT6; Site 1: Noti;
Site_2: Sall; transgenic model WNT-1, expression driver
MMTV-LFR enhancer; Cloned unidirectionally. Primer: Ol
dT. Library constructed by Life Technologies
dT. Library constructed by Life Technologies
Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                             tissue_type="tumor, metastatic to mammary"
                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:4020600"
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83.9%;
                        57.5%;
74.4%;
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Score 23; DB 2; Lo
Pred. No. 2.3e+02;
0; Mismatches 10;
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Pred. No. 2.2e+02;
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د.
                                                 Length 968;
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BM406466
LOCUS
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ORGANISM
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AUTHORS
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Best Local
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                                                                                                                                                                                                                             649
Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                               Bequence.
AW257178
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                                                                                                                                                                                                                                                                                             27;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
asterids; lamiids; Solanales; Solanaceae; Solanum.
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EST580781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: potato-array@tigr.org
This clone can be obtained from the Univer
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Robin Buell
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ror Tankeley,S. and Baker,B. Generation of ESTs from potato roots
                                                                 AW257178.1 GI:6605435
EST.
                                                                                                                            EST305315 KV2 Medicago truncatula
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Solanum tuberosum (potato)
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BM406466.1 GI:18258084
                                                                                                                                              AW257178
                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                             TCCCTCCTTCCACACAATCCACCATACTCAAGCA 682
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                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                  /clone lib="potato roots"
/clone lib="potato roots"
/note="Vector: pBluescript SK(-); Site_1: EcoRT; Site_2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing; The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Solanum tuberosum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potato roots Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dev stage="in vitro grown stem cuttings"
lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:4113"
clone="cPRO27F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="roots"
                                                                                                                                                                                                                                                                                                         57.0%;
79.4%;
                                                                                                                                                                                                                                                                                          ; Score 22.8; Di
; Pred. No. 2.6e
0; Mismatches
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.6e+02;
                                                                                                                             cDNA clone
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n cDNA clone
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                                                                                                                             linear EST 20-DEC-1999
ne KV2-7D15, mRNA
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CPRO27F14 5'
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BE205271
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                                 COMMENT
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Best Local S
Matches 25
                                               TITLE
JOURNAL
                                                                                                                                                                                                           ORGANISM
                                                                                                              AUTHORS
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BE205271
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Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
                                                                     ESTs from uninoculated seedling 
Unpublished (1999)
                                                                                                                                           VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE205271 560 bp
EST397947 KV0 Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kvandenb@cbs.umn.edu
Texas A&M EST name:T115883e
TIGR sequence name:MTAAO20TK
More information is availble at...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Minnesota
220 BioSci Center, 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: VandenBosch K
Department of Plant Biology
                                                                                                                       Town, C.D., Bowman, C.L.,
Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 612 624 2755
Fax: 612 625 1738
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Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. coli strain SOLR"
/clone lib="KY2"
/clone lib="KY2"
/note="Vector: pBBuescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Glapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ex-assist helper phage and propagated in SOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype_A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="KV2-7D15"
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Pred. No. 2.8e+02;
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                                                                                                 roots of Medicago truncatula
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pKV0-21123, mRNA
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, Holt,I.E. and
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Search completed: September 16, 2005, 08:08:40 Job time : 131.754 secs
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                                                                                                                                                                                                        Query Match
Best Local Similarity 86.2
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                        24 ACCAACTCCCAAACAATCAATCGTGCTCA 52
                                                                                                                                      6 ACCTACTCCCAAACAATCCATCTTACTCA 34
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Fax: 612 625 1738
Email: kvandenb@cbb.umn.edu
Texas A&M University name:T265043e
TIGR sequence name:MTGBK60TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/mol type="mRNA"
/cultIvar="genotype A17"
/db xref="genotype A17"
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SinorNizobium meliloti (0 hour)"
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/clone lib="KV0"
/clone lib="KV0"
/clone lib="KV0"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack II Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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86.2%;
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Pred. No. 3e+02;
0; Mismatches 4;
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